



**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application No.: 09/857,128

Applicant: MURDIN, Andrew D. et al.

Filed: September 20, 2001

TC/A.U.: 1645

Examiner: Nita M. Minnifield

Docket No: 032931/0252

**DECLARATION PURSUANT TO 37 CFR 1.131**

I, Andrew Murdin, Director, External R&D Canada, Aventis Pasteur, hereby declare that:

1. I am an inventor in the above-identified application, and am employed by the assignee, Aventis Pasteur.

2. Details of my employment history are as follows:

Since 2002 Director, External R&D Canada, Aventis Pasteur.

1999-2002 Principal Research Scientist, Aventis Pasteur.

1997-2002 Section Head, Aventis Pasteur.

1993-2003 Project Leader (Chlamydia), Aventis Pasteur.

1990-1993 Research Scientist, Connaught Laboratories Ltd. (subsequently Pasteur Merieux Connaught, subsequently Aventis Pasteur), Toronto, Canada.

1988-1990 Post-Doctoral Research Associate, Dept. of Microbiology, State University of New York, Stony Brook, NY, USA.

1985-1987 Post-Doctoral Research Fellow, Dept. of Microbiology, University of Surrey, Guildford, Surrey, England.

1981-1985 Scientific Officer, Vaccine Research Dept., Animal Virus Research Institute, Pirbright, Surrey, England.

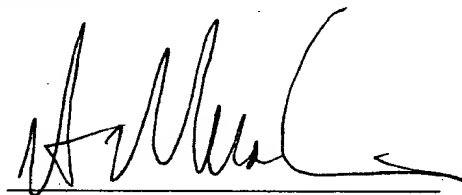
Details of my education are as follows:

B.Sc., University of Bath, England, 1980

Ph.D., University of Surrey, England, 1986.

3. Attached is a copy of a document signed by me and Dathao Ho, an employee of the assignee Aventis Pasteur. The document sets forth the amino acid sequence, the nucleotide sequence, and the restriction map of CPN100638.
4. CPN100638 corresponds to the gene identified as SEQ ID Nos: 5, 6 and 14 of the application. The amino acid sequence of CPN100638 set forth in the attached document is identical to SEQ ID No:14 of this application. The sequences and restriction map are essentially the same as Figures 5 and 6 of the application.
5. The document was redacted to remove information other than the sequences. The dates deleted from the attached document are before November 4, 1998.
6. The document shows that I possessed these amino acid and nucleotide sequences prior to November 4, 1998.
7. I hereby declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.

4<sup>th</sup> March 2004  
Date

  
Andrew Murdin

Director, External R&D Canada, Aventis Pasteur

## CONFIDENTIAL

>CPN100638 putative 98 kDa outer membrane protein  
MKSSLHWFLISSSLALPLSLNFSFAFAAVVEINLGPTNSFSGPGTYTPPAQTTNADGTIYNLTGDVSITNAGSPTA  
LTASCFKETTGNLSFQGHGYQFLLQNI DAGANCTFTNTAANKLLSFGFSYLSLIQTTNATTGTGAIKSTGACSI  
QSNYSCYFGQNFNDNGGALQGSSISLSLNPNTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANNNGGA  
IYTEASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDN GELNFIGNTAITSGGAIYTDNLVLSS  
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LKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVDLSLKETKKGTLKATQASQTVTLSGSLSLVDPS  
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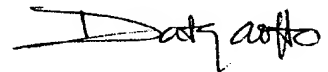
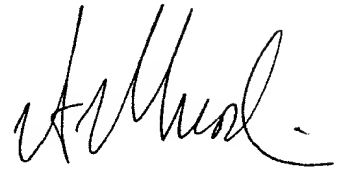
### CODING SEQUENCE

THE SEQUENCE IS ENCODED ON THE NEGATIVE STRAND

The ATG is presumably the start codon

The TAA is presumably the stop codon

1 TGTAGATTCT TAACTTACTA GTCTCTCCTT TCCTCTTGCT TTCTTTAATT  
51 TATTGCAGTA TGTGGTGAAA TAATTTGTTA AACCACCTAT AGCCCTCTAC  
101 ATGAATCCT CTCTTCATTG GTTTTTAATC TCGTCATCTT TAGCACTTCC  
151 CTTGTCACCTA AATTTCTCTG CGTTTGCTGC TGTTGTGAA ATCAATCTAG  
201 GACCTACCAA TAGCTTCTCT GGACCAGGAA CCTACACTCC TCCAGCCCAA  
251 ACAACAAATC CAGATCGAAC TATCTATAAT CTAACAGCCC ATCTCTCAAT  
301 CACCAATGCA GGATCTCCGA CAGCTCTAAC CGCTTCCTGC TTAAAGAAA  
351 CTACTGGGAA TCTTTCTTTC CAAGGCCACG GCTACCAATT TCTCCTACAA  
401 AATATCGATG CGGGAGCGAA CTGTACCTTT ACCAATACAG CTGCAAATAA  
451 GCTTCTCTCC TTTTCAGGAT TCTCCTATTT GTCACAAATA CAAACCACGA  
501 ATGCTACCAC AGGAACAGGA GCCATCAAGT CCACAGGAGC TTGTTCTATT  
551 CAGTCGAAT ATAGTTGCTA CTTTGGCCAA AACTTTTCTA ATGACAATGG  
601 AGGCGCCCTC CAAGGCAGCT CTATCAGTCT ATCGCTAAAC CCCAACCTAA  
651 CGTTTGCCAA AAACAAAGCA ACGCAAAAAG GGGGTGCCCT CTATTCCACG  
701 GGAGGGATTA CAATTAACAA TACGTTAAAC TCAGCATCAT TTTCTGAAAA  
751 TACCGCGGCG AACAAATGGCG GAGCCATTTA CACGGAAGCT AGCAGTTTTA



801 TTAGCAGCAA CAAAGCAATT ACCTTTATAA ACAATAGTGT GACCGCAACC  
 851 TCAGCTACAG GGGGAGCCAT TTACTGTAGT AGTACATCAG CCCCCAAACC  
 901 AGTCTTAACT CTATCAGACA ACGGGGAAC TGAACCTTATA GGAAATACAG  
 951 CAATTACTAG TGGTGGGGCG ATTTATACTG ACAATCTAGT TCTTTCTTCT  
 1001 GGAGGACCTA CGCTTTTTAA AAACAAC TCT GGCTATGATA CTGCAGCTCC  
 1051 CTTAGGAGGA GCAATTGCGA TTGCTGACTC TGGATCTTTG AGTCTTTTCG  
 1101 CTCTTGGTGG AGACATCACT TTTGAAGGAA ACACAGTAGT CAAAGGAGCT  
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 1301 TTAAATGGTC CTGACCTTGC AGGGAATCCT GCATATCAAG GAACCATCGT  
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 1401 TCAAATCTAC AATTCAGCAA CCTCTAATC TTGCGGGAGG GCAACTCTCT  
 1451 CTTAAATCAG GAGTCACTCT AGTTGCTAAG TCCTTTTCGC AATCTCCGGG  
 1501 CTCTACCCTC CTCATGGATG CAGGGACCAC ATTAGAAACC GCTGATGGGA  
 1551 TCACTATCAA TAATCTTGTT CTCAATGTAG ATTCTTTAAA AGAGACCAAG  
 1601 AAGGGCACGC TAAAAGCAAC ACAAGCAAGT CAGACAGTCA CTTTATCTGG  
 1651 ATCGCTCTCT CTTGTAGATC CTTCTGGAAA TGTCTACGAA GATGTCTCTT  
 1701 GGAATAACCC TCAAGTCTTT TCTTGTCTCA CTCTTACTGC TGACGACCCC  
 1751 GCGAATATTC ACATCACAGA CTTAGCTGCT GATCCCCTAG AAAAAATCC  
 1801 TATCCATTGG GGATACCAAG GGAATTGGGC ATTATCTTGG CAAGAGGATA  
 1851 CTGCGACTAA ATCCAAAGCA GCGACTCTTA CCTGGACAAA AACAGGATAC  
 1901 AATCCGAATC CTGAGCGTCG TGGAACCTTA GTTGCTAACA CGCTATGGGG  
 1951 ATCCTTTGTT GATGTGCGCT CCATACAACA GCTTGTAGCC ACTAAAGTAC  
 2001 GCCAATCTCA AGAAACTCGC GGCATCTGGT GTGAAGGGAT CTCGAAC TTC  
 2051 TTCCATAAAG ATAGCACGAA GATAAATAAA GGTTTTTCGCC ACATAAGTGC  
 2101 AGGTTATGTT GTAGGAGCGA CTACAACATT AGCTTCTGAT AATCTTATCA  
 2151 CTGCAGCCTT CTGCCAATTA TTCGGGAAAG ATAGAGATCA CTTTATAAAT  
 2201 AAAAATAGAG CTTCTGCCTA TGCAGCTTCT CTCCATCTCC AGCATCTAGC



2251 GACCTTGTCT TCTCCAAGCT TGTTACGCTA CCTTCCTGGA TCTGAAAGTG  
2301 AGCAGCCTGT CCTCTTTGAT GCTCAGATCA GCTATATCTA TAGTAAAAAT  
2351 ACTATGAAAA CCTATTACAC CCAAGCACCA AAGGGAGAGA GCTCGTGGTA  
2401 TAATGACGGT TCGCTCTGG AACTTGCGAG CTCCCTACCA CACACTGCTT  
2451 TAAGCCATGA GGGTCTCTTC CACGCGTATT TTCCTTTCAT CAAAGTAGAA  
2501 GCTTCGTACA TACACCAAGA TAGCTTCAA GAACGTAATA CTACCTTGGT  
2551 ACGATCTTTC GATAGCGGTG ATTTAATTAA CGTCTCTGTG CCTATPGGAA  
2601 TTACCTTCGA GAGATTCTCG AGAAACGAGC GTGCGTCTTA CGAAGCTACT  
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2801 CTTGAGGTCA CAAGTAACCT ATCTATGGAA ATTCGTGGAT CTTACGCAG  
2851 CTACAATGCA GATCTTGGAG GTAAGTTCCA GTTCTAAAAG CGTTCCTGAT  
2901 CCCTTAGAAA TTCTAAGAGA TCCTGAGTGT ATCTAGGGAC TTCTCAAAGA

# SEQUENCE ALIGNMENT

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  1 MetLysSerSerLeuHisTrpPheLeuileSerSerSerLeuAlaLeuPr 17

151 CTTGTCACTAAATTTCTCTGCGTTTGCTGCTGTGTTGAAATCAATCTAG 200
    ||||||||||||||||||||||||||||||||||||||||||||||||
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251 ACAACAAATGCAGATGGAACCTATCTATAATCTAACAGGGGATGTCTCAAT 300
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301 CACCAATGCAGGATCTCCGACAGCTCTAACCCTTCTCTGCTTTAAAGAAA 350
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351 CTACTGGGAATCTTTCTTTCCAAGGCCACGGCTACCAATTTCTCCTACAA 400
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  85 hrThrGlyAsnLeuSerPheGlnGlyHisGlyTyrGlnPheLeuLeuGln 100

401 AATATCGATGCGGGAGCGAACTGTACCTTTACCAATACAGCTGCAAATAA 450
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451 GCTTCTCTCTTTTTCAGGATTTCTCCTATTGTGCTACTAATACAAACCACGA 500
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118 sLeuLeuSerPheSerGlyPheSerTyrLeuSerLeuIleGlnThrThrA 134

501 ATGCTACCACAGGAACAGGAGCCATCAAGTCCACAGGAGCTTGTTCATT 550
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135 snAlaThrThrGlyThrGlyAlaIleLysSerThrGlyAlaCysSerIle 150

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601 AGGCGCCCTCCAAGGCAGCTCTATCAGTCTATCGCTAAACCCCAACCTAA 650
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168 yGlyAlaLeuGlnGlySerSerIleSerLeuSerLeuAsnProAsnLeuT 184

651 CGTTTGCCAAAAACAAAGCAACGCAAAAAGGGGGTGCCCTCTATTCCACG 700
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185 hrPheAlaLysAsnLysAlaThrGlnLysGlyGlyAlaLeuTyrSerThr 200

701 GGAGGGATTACAATTAACAATACGTTAAACTCAGCATCATTTTCTGAAAA 750
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201 GlyGlyIleThrIleAsnAsnThrLeuAsnSerAlaSerPheSerGluAs 217

751 TACCGCGGCGAACAATGGCGGAGCCATTTACACGGAAGCTAGCAGTTTTA 800
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|||||
401 LeuAsnGlyProAspLeuAlaGlyAsnProAlaTyrGlnGlyThrIleVa 417
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418 lPheSerGlyGluLysLeuSerGluAlaGluAlaAlaGluAlaAspAsnL 434
|||||
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|||||
435 euLysSerThrIleGlnGlnProLeuThrLeuAlaGlyGlyGlnLeuSer 450
|||||
1451 CTTAAATCAGGAGTCACTCTAGTTGCTAAGTCCTTTTCGCAATCTCCGGG 1500
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451 LeuLysSerGlyValThrLeuValAlaLysSerPheSerGlnSerProGl 467

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2201 AAAAATAGAGCTTCTGCCTATGCAGCTTCTCTCCATCTCCAGCATCTAGC 2250

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2301 AGCAGCCTGTCTCTTTGATGCTCAGATCAGCTATATCTATACTAAAAAT 2350
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2401 TAATGACGGTTCGCGCTCTGGAACCTTGCGAGCTCCCTACCACACACTGCTT 2450
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768 rAsnAspGlyCysAlaLeuGluLeuAlaSerSerLeuProHisThrAlaL 784
2451 TAAGCCATGAGGGTCTCTTCCACGCGTATTTTCCTTTTCATCAAAGTAGAA 2500
|||||
785 euSerHisGluGlyLeuPheHisAlaTyrPheProPheIleLysValGlu 800
2501 GCTTCGTACATACACCAAGATAGCTTCAAAGAACGTAATACTACCTTGGT 2550
|||||
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835 leThrPheGluArgPheSerArgAsnGluArgAlaSerTyrGluAlaThr 850
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2751 GACAAGCTGGTATCGGAAGAGCAGGGATCTTTTATGCCTTCTCTCCAAAT 2800
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885 rgGlnAlaGlyIleGlyArgAlaGlyIlePheTyrAlaPheSerProAsn 900
2801 CTTGAGGTCAACAAGTAACCTATCTATGGAAATTCGTGGATCTTCACGCAG 2850
|||||
901 LeuGluValThrSerAsnLeuSerMetGluIleArgGlySerSerArgSe 917
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918 rTyrAsnAlaAspLeuGlyGlyLysPheGlnPhe 928

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### RESTRICTION MAP

HinfI                BfaI                          Tsp509I  
TfiII MseI SpeI BsmAI MnII CviRI

TGTAGATTCTTAAC TTACTAGTCTCTCCTTTCC TCTTGCTTTCTTTAATTTATTGCAGTA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ACATCTAAGAATTGAATGATCAGAGAGGAAAGGAGAACGAAAGAAATTAAATAACGTCAT

MboII  
MseI MnII MnII  
Tsp509I HphI SfcI NlaIII EarI

TGTGGTGAAATAATTTGT TAAACCACCTATACCCCTCTACATGAAATCCTCTCTTCAT TG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ACACCACTTTATTAAACAATTTGGTGGATATCGGGAGATGTACTTTAGGAGAGAAGTAAC

BbvI  
ApoI Tsp509I Fnu4HI  
MaeIII Tsp45I MwoI TseI

MseI

GTTTTTAATCTCGTCATCTTTAGCACTTCCCCTTG TCACTAAATTTCTCTGCGTTTGTCTGC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
CAAAAATTAGAGCAGTAGAAATCGTGAAGGGAACAGTGATTTAAAGAGACGCAAACGACG

NlaIV  
BseRI  
BpmI ScrFI  
EcoRII  
AvaII AvaII BspGI Sau96I  
Hpy178III BsaXI  
AluI AluI PpiI  
CviJI

TGTTGTTGAAATCAATCTAGGACCTACCAATAGCTT CTCTGGACCAGGAACCTACACTCC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ACAACA ACTTTAGTTAGATCCTGGATGGTTATCGAAGAGACCTGGTCTTG GATGTGAGG

BccI  
MnII Tth111III  
CviJI CviRI HphI BsmAI

TCCAGCCCCAAACA ACAAATGCAGATGGA ACTATCTATAATCTAACAGGGGATGTCTCAAT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
AGGTCGGGTTTGT GTTTACGTCTACCTTG ATAGATATTAGATTGTCCCCTACAGAGTTA

AluI  
CviJI  
AlwI  
Hpy188IX DpnI BsrI

Diagram illustrating the restriction enzyme sites for various enzymes across four DNA fragments (301-360, 361-420, 421-480, 481-540) and their corresponding sequences.

**Fragment 301-360:**

Enzymes: FokI, BstYI, Sau3AI, CviRI, AceIII, MwoI, DraI, MseI, MmeI, HinfI, TfiI, BmrI.

Sequence:  
CACCAATGCAGGATCTCCGACAGCTCTAACCGCTTCCTGCTTTAAAGAAACTACTGGGAA  
GTGGTTACGTCCTAGAGGCTGTCTGAGATTGGCGAAGGACGAAATTTCTTTTGATGACCCTT

**Fragment 361-420:**

Enzymes: BsaJI, BstDSI, CviJI, HaeI, HaeIII, StryI, Tsp509I, CviJI, SfaNI, BceFI, Sth132I, ClaI, TaqI, FauI, AcII.

Sequence:  
TCTTTCTTTTCCAAGGCCACGGCTACCAATTTCTCTCTACAAAATATCGATGCGGGAGCGAA  
AGAAAGAAAGGTTCCGGTGCCGATGGTTAAAGAGGATGTTTTATAGCTACGCCCTCGCTT

**Fragment 421-480:**

Enzymes: RsaI, BbvI, TaaI, Fnu4HI, AluI, CviJI, MspAI, PvuII, TseI, HindIII, CviJI, AluI, Hpy178III, HinfI, TfiI, MaeIII, Tsp45I.

Sequence:  
CTGTACCTTTTACCAATACAGCTGCAAATAAGCTTCTCTCTTTTCAGGATTCTCTCTATTT  
GACATGGAAATGGTTATGTCTGACGTTTATTTCGAAGAGAGGAAAAGTCCTAAGAGGATAAA

**Fragment 481-540:**

Enzymes: BsmI, BccI, CviJI, NlaIV, AluI, CviJI.

Sequence:  
GTCAC TAATACAAACCACGAATGCTACCAACAGGAACAGGACCATCAAGTCCACAGGAGC  
CAGTGATTATGTTTGGTGCTTACGATGGTGTCTTGTCTCGGTAGTTTCAGGTGTCTCTCG

**Fragment 541-600:**

Enzymes: CviJI, HaeI, HaeIII, MscI, EaeI, MwoI, TaqI, SfcI, CjePI, MnII, BsaJI, HaeII.

Sequence:  
TTGTCTATTTCAGTCGAAC TATAGTTGCTACTTTGGCCAAA ACTTTTCTAATGACAATGG  
AACAAGATAAGTCAGCTTGATATCAACGATGAAACCGGTTTTTGAAAAGATTACTGTTACC

HhaI |  
 Hin4I |  
 NlaIV |  
 BsaHI |  
 NarI |  
 BanI |  
 CjePI |  
 AluI |  
 CviJI |  
 MnlI |  
 Fnu4HI |  
 StyI |  
 TseI |  
 BplI |  
 AceIII |  
 BbvI |  
 CjePI |  
 AclI |  
 MaeII |  
 AGGCGCCCTCCAAGGCAGCTCTATCAGTCTATCGCTAAACCCCAACCTAACGTTTGCCAA  
 601 -----+-----+-----+-----+-----+ 660  
 TCCGCGGGAGGTTCCGTCGAGATAGTCAGATAGCGATTGGGGTTGGATTGCAAACGGTT

Sth132I |  
 Bsp1286I |  
 BmgI |  
 BseSI |  
 NlaIV |  
 BanI |  
 BscGI |  
 MnlI |  
 BsaJI |  
 BstDSI |  
 MnlI |  
 BslI |  
 MseI |  
 Tsp509I |  
 AAACAAAGCAACGCAAAAAGGGGTGCCCTCTATTCCACGGGAGGGATTACAATTAACAA  
 661 -----+-----+-----+-----+-----+ 720  
 TTTGTTTCGTTGCGTTTTTCCCCACGGGAGATAAGGTGCCCTCCCTAATGTTAATTGTT

Fnu4HI |  
 SacII |  
 TauI |  
 AciI |  
 MspAII |  
 ThaI |  
 BseMII |  
 Hpy188IX |  
 SfaNI |  
 BstDSI |  
 MaeII |  
 DdeI |  
 CviJI |  
 NlaIV |  
 EciI |  
 AciI |  
 TACGTTAAACTCAGCATCATTTTCTGAAAATACCGCGCGAACAATGGCGGAGCCATTTA  
 721 -----+-----+-----+-----+-----+ 780  
 ATGCAATTTGAGTCGTAGTAAAAGACTTTTATGGCGCCGCTTGTTACCGCCTCGGTAAAT

Cac8I |  
 BfaI |  
 AluI |  
 CviJI |  
 NheI |  
 Fnu4HI |  
 TseI |  
 BbvI |  
 Tsp509I |  
 AluI |  
 CviJI |  
 MaeIII |  
 Tsp45I |  
 CACGGAAGCTAGCAGTTTATTAGCAGCAACAAAGCAATTAGCTTTATAAACAATAGTGT  
 781 -----+-----+-----+-----+-----+ 840  
 GTGCC TTCGATCGTCAAAATAATCGTCGTTGTTTCGTTAATCGAAATATTGTTATCACA

CviJI |  
 NlaIV |  
 BseMII |  
 MnlI |  
 CjeI |  
 SfcI |  
 AluI |  
 CviJI |  
 MwoI |  
 BbvCI |



[illegible]

| | | | | | | | | |  
 CAAAGGAGCTTCTTCGAGTCAGACCACTACCAGAAATTCTATTAACATCGGAAACACCAA  
 1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
 GTTTCCTCGAAGAAGCTCAGTCTGGTGATGGTCTTTAAGATAATTGTAGCCTTTGTGGTT

CviJI  
 Cac8I  
 Fnu4HI  
 AluI  
 CviJI  
 MspAII  
 PvuII  
 Bce83I  
 RsaI  
 BbvI BsrGI  
 DdeI TatI TseI SmlI MnlI AlwI Sau3AI DpnI  
 TGCTAAGATTGTACAGCTGCGAGCCTCTCAAGGCAATACTATCTACTTCTATGATCCTAT  
 1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
 ACGATTCTAACATGTCGACGCTCGGAGAGTTCCGTTATGATAGATGAAGATACTAGGATA

AceIII  
 BbvI  
 Hpy188IX  
 AluI  
 CviJI  
 PstI  
 SfaNI  
 TspRI  
 Fnu4HI  
 SfaNI  
 CviRI  
 TseI  
 BtsI  
 BfaI SfcI DdeI Hpy178III MseI AvaII  
 BseMII Sau96I CviRI  
 AACAACTAGCATCACTGCAGCTCTCTCAGATGCTCTAAACTTAAATGGTCCTGACCTTGC  
 1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
 TTGTTGATCGTAGTGACGTCGAGAGAGTCTACGAGATTTGAATTTACCAGGACTGGAACG

Hpy188IX  
 BbvI  
 AluI  
 CviJI  
 HinfI BccI  
 TfiI DrdII  
 CviRI NlaIV Hpy178III Hin4I BpmI  
 AGGGAATCCTGCATATCAAGGAACCATCGTATTTTCTGGAGAGAAGCTCTCGGAAGCAGA  
 1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
 TCCCTTAGGACGTATAGTTCCCTTGGTAGCATAAAAGACCTCTCTTCGAGAGCCTTCGTCT

AluI  
 AlwNI  
 CviJI  
 MwoI  
 PstI  
 CviRI

Bp1I  
 Fnu4HI  
 SfcI  
 AluI  
 AlwNI  
 Bp1I  
 BstAPI  
 CviJI  
 MwoI  
 TseI  
 Tsp509I  
 FauI  
 MnlI  
 Sth132I  
 MnlI  
 AcII  
 1381  
 AGCTGCAGAAGCTGATAATCTCAAATCTACAATTCAGCAACCTCTAATCTTGCGGGAGG  
 TCGACGTCTTCGACTATTAGAGTTTAGATGTTAAGTCGTTGGAGATTGAGAACGCCCTCC  
 1440  
 MaeIII  
 Tsp45I  
 HinfI  
 Bp1I  
 Hpy178III  
 BfaI  
 PleI  
 DdeI  
 Sth132I  
 CviJI  
 BseRI  
 NciI  
 ScrFI  
 MspI  
 Hin4I  
 MseI  
 1441  
 GCAACTCTCTCTTAAATCAGGAGTCACTCTAGTTGCTAAGTCCTTTTCGCAATCTCCGGG  
 CGTTGAGAGAGAATTTAGTCCTCAGTGAGATCAACGATTCAGGAAAAGCGTTAGAGGCC  
 1500  
 FokI  
 CjeI  
 NlaIV  
 AvaII  
 Sau96I  
 CviRI  
 MnlI  
 SfaNI  
 MnlI  
 NlaIII  
 BslI  
 BanII  
 Bsp1286I  
 MspAI  
 Sau3AI  
 BccI  
 BsmFI  
 BslI  
 DpnI  
 BsaBI  
 AlwI  
 1501  
 CTCTACCCTCCTCATGGATGCAGGGACCACATTAGAAACCGCTGATGGGATCACTATCAA  
 GAGATGGGAGGAGTACCTACGTCCCTGGTGTAACTTTGGCGACTACCCTAGTGATAGTT  
 1560  
 Bsp1286I  
 Cac8I  
 BmgI  
 BseSI  
 BsaI  
 HinfI  
 BsmAI  
 TfiI  
 MseI  
 CjeI  
 1561  
 TAATCTTGTTCTCAATGTAGATTCCCTTAAAAGAGACCAAGAAGGCACGCTAAAAGCAA  
 ATTAGAACAAGAGTTACATCTAAGGAATTTCTCTGGTTCTTCCCGTGCGATTTTCGTTG  
 1620  
 Hpy178III  
 DpnI  
 BstYI  
 Sau3AI  
 CjeI  
 AlwI  
 Hpy188IX  
 CjeI  
 MwoI  
 Tth111III  
 MaeIII  
 TaaI  
 Tsp45I  
 DpnI  
 Sau3AI  
 Hpy178III  
 AlwI

| | | | | | | | | |  
 ACAAGCAAGTCAGACAGTCACCTTTATCTGGATCGCTCTCTCTGTAGATCCTTCTGGAAA  
 1621 -----+-----+-----+-----+-----+-----+ 1680  
 TGTTCGTTTCAGTCTGTCTAGTCAAATAGACCTAGCGAGAGAGAACATCTAGGAAGACCTTT

Pfl1108I                      MboII  
 AccI                      BsmAI                      CjePI  
 CjePI                      Bce83I                      SmlI                      MnlI                      BsmAI  
 | | | | | | | | | |  
 TGTCTACGAAGATGTCTCTTGGGAATAACCTCAAGTCTTTTCTGTCTCACTCTTACTGC  
 1681 -----+-----+-----+-----+-----+-----+ 1740  
 ACAGATGCTTCTACAGAGAACCTTATTGGGAGTTCAGAAAAGAACAGAGTGAGAATGACG

DpnI  
 Sau3AI  
 Fnu4HI  
 AluI  
 AlwI  
 CviJI  
 TseI  
 FauI  
 SspI  
 Sth132I  
 ThaI  
 SimI    AciI                      BbvI                      DdeI                      BfaI  
 | | | | | | | | | |  
 TGACGACCCCGCGAATATTCACATCACAGACTTAGCTGCTGATCCCCCTAGAAAAAATCC  
 1741 -----+-----+-----+-----+-----+-----+ 1800  
 ACTGCTGGGGCGCTTATAAGTGTAGTGTCTGAATCGACGACTAGGGGATCTTTTTTTAGG

Tsp509I  
 BciVI                      BsaJI                      BciVI  
 StyI                      MnlI  
 | | | | | | | | | |  
 TATCCATTGGGGATACCAAGGGAATTGGGCATTATCTTGGCAAGAGGATACTGCGACTAA  
 1801 -----+-----+-----+-----+-----+-----+ 1860  
 ATAGGTAACCCCTATGGTTCCCTTAACCCGTAATAGAACCGTTCTCCTATGACGCTGATT

Bpu10I  
 DdeI  
 Hpy178III  
 HinfI  
 TfiI  
 HgaI  
 Hpy188IX  
 BseMII  
 HinfI                      BspGI  
 Fnu4HI                      ScrFI  
 TseI                      BbvI  
 PleI                      EcoRII                      BciVI  
 | | | | | | | | | |  
 ATCCAAAGCAGCGACTCTTACCTGGACAAAAACAGGATACAATCCGAATCCTGAGCGTCG  
 1861 -----+-----+-----+-----+-----+-----+ 1920  
 TAGGTTTCGCTCGCTGAGAATGGACCTGTTTTTGTCTATGTTAGGCTTAGGACTCGCAGC

DpnI  
 NlaIV  
 BamHI  
 BstYI  
 Sau3AI  
 AlwI                      AlwI                      CjeI  
 CjeI  
 DdeI  
 NlaIV                      HhaI  
 | | | | | | | | | |  
 TGGAACTTAGTTGCTAACACGCTATGGGGATCCTTTGTTGATGTGCGCTCCATACAACA  
 1921 -----+-----+-----+-----+-----+-----+ 1980  
 ACCTTGGAATCAACGATTGTGCGATACCCCTAGGAAACAACACGCGAGGTATGTTGT

AluI Bce83I Hpy178III Fnu4HI DpnI  
CviJI CviJI RsaI SmlI TauI AcilI BstYI  
SfaNI Sau3AI

GCTTGTAGCCACTAAAGTAGCCAATCTCAAGAACTCGGGCATCTGGTGTGAAGGGAT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
CGAACATCGGTGATTTCATGCGGTTAGAGTTCTTTGAGCGCCGTAGACCACACTTCCCTA

XmnI  
AlwI  
Hpy178III  
TaqI  
MboII MboII BspMI MslI CviRI

CTCGAACTTCTTCCATAAAGATAGCACGAAGATAAATAAAGGTTTTTCGCCACATAAGTGC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GAGCTTGAAGAAGGTATTCTATCGTGCTTCTATTTATTTCCAAAGCGGTGTATTACGC

CviJI PstI TspRI  
Fnu4HI  
CviRI  
Hpy188IX  
TseI  
BtsI  
SfcI

BsgI AluI CviJI

AGGTTATGTGTAGGAGCGACTACAACATTAGCTTCTGATAATCTTATCACTGCAGCCTT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TCCAATACAACATCCTCGCTGATGTTGTAATCGAAGACTATTAGAATAGTGACGTCGGAA

BbvI DpnI  
Tsp509I Sau3AI  
Sth132I Hpy178III BsaBI AluI  
CviJI

CTGCCAATTATTCGGGAAAGATAGAGATCAC TTATAAATAAAAAATAGAGCTTCTGCCTA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GACGGTTAATAAGCCCTTCTATCTCTAGTGAAATATTTATTTTATCTCGAAGACGGAT

AluI  
CviJI  
Fnu4HI  
BpmI  
CviRI  
MwoI  
TseI

Tth111I  
SfaNI  
BbsI  
MboII  
BfaI

MaeIII  
AluI  
CviJI  
HindIII

BbvI  
BccI

TGCAGCTTCTCTCCATCTCCAGCATCTAGCGACCTTGCTCTTCTCCAAGCTTGTTACGCTA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ACGTCGAAGAGAGGTAGAGGTCGTAGATCGCTGGAACAGAAGAGGTTCGAACAATGCGAT

SfcI  
BseMII  
AluI  
CviJI

Hpy188IX

DpnI  
 BstYI  
 Sau3AI  
 ScrFI  
 EcoRII  
 DpnI  
 SfaNI  
 CviJI  
 Fnu4HI  
 TseI  
 AluI  
 BbvI  
 DpnI  
 Sau3AI  
 Hpy188IX  
 DdeI  
 MnlI  
 2281  
 CCTTCCTGGATCTGAAAGTGAGCAGCCTGTCTCTTTGATGCTCAGATCAGCTATATCTA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340  
 GGAAGGACCTAGACTTTTACTCGTCGGACAGGAGAACTACGAGTCTAGTCGATATAGAT  
 BanII  
 BsiHKA  
 Bsp1286I  
 SacI  
 RssSI  
 AluI  
 CviJI  
 Tth111III  
 CjePI  
 TaqII  
 2341  
 TAGTAAAAATACTATGAAAACCTATTACACCCAAGCACCAAAGGGAGAGAGCTCGTGGTA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400  
 ATCATTTTATGATACTTTTGGATAATGTGGGTTCGTGGTTTCCCTCTCTCGAGCACCAT  
 BanII  
 BsiHKA  
 Bsp1286I  
 SacI  
 Hpy178III  
 HhaI  
 CjePI  
 TaaI  
 AluI  
 CviJI  
 Cac8I  
 CviJI  
 MnlI  
 MseI  
 TspRI  
 BtsI  
 NlaIII  
 MboII  
 2401  
 TAATGACGGTTGCGCTCTGGAAC\*TTGCGAGCTCCCTACCACACTGCTTTAAGCCATGA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460  
 ATTACTGCCAACGCGAGACCTTGAACGCTCGAGGGATGGTGTGTGACGAAATTTCGGTACT  
 Thai  
 AflIII  
 MluI  
 EarI  
 BsaI  
 SimI  
 BsmAI  
 AluI  
 CviJI  
 HindIII  
 RsaI  
 2461  
 GGGTCTCTTCCACGCGTATTTTCCTTTTCATCAAAGTAGAAGCTTCGTACATACACCAAGA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520  
 CCCAGAGAAGGTGCGCATAAAGGAAAGTAGTTTCATCTTCGAAGCATGTATGTGGTTCT  
 MaeII  
 HphI  
 MseI  
 PacI  
 DpnI  
 BsaJI  
 Sau3AI  
 StyI  
 RsaI  
 TaqI  
 AciI  
 Tsp509I  
 MseI  
 AluI  
 CviJI  
 MaeII  
 2521  
 TAGCTTCAAAGAACGTAATACTACCTTGGTACGATCTTTTCGATAGCGGTGATT\*TAATTAA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580  
 ATCGAAGTTTCTTGCATTATGATGGAACCATGCTAGAAAGCTATCGCCACTAAATT\*TAATT

HpaI  
 Hpy178III  
 Hpy178III  
 TaqI  
 AvaI  
 SmlI  
 HinfI  
 HinfI  
 BspI  
 BsmAI  
 BsmBI  
 Tsp509I  
 Hpy178III  
 TaqI  
 TfiI  
 XhoI  
 Cac8I  
 HinfI  
 CGTCTCTGTGCCTATTGGAATTACCTTCGAGAGATTCTCGAGAAACGAGCGTGCCTCTTA  
 2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640  
 GCAGAGACACGGATAACCTTAATGGAAGCTCTCTAAGAGCTCTTTGCTCGCACGCAGAAT  
 Hpy178III  
 AluI  
 CviJI  
 TaaI  
 MaeII  
 BsaBI  
 BsgI  
 HinfI  
 TfiI  
 CviRI  
 AluI  
 CviJI  
 CGAAGCTACTGTCTATCTACGTTGCCGATGTCTATCGTAAGAATCTTGACTGCACGACAGC  
 2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700  
 GCTTCGATGACAGTAGATGCAACGGCTACAGATAGCATTCTTAGGACTGACGTGCTGTGCG  
 Bce83I  
 SfcI  
 HinfI  
 TfiI  
 SmlI  
 AluI  
 CviJI  
 AceIII  
 BssSI  
 MnlI  
 TCTCCTAATCAACAATACCTCGTGGAAGTACAGGAACGAATCTCTCAAGACAAGCTGG  
 2701 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760  
 AGAGGATTAGTTGTTATGGAGCACCTTTTGATGTCTCTTGCTTAGAGAGTTCTGTTCGACC  
 MboII  
 DpnI  
 Hpy188IX  
 EarI  
 SapI  
 BstYI  
 Sau3AI  
 HinfI  
 AlwI  
 Hpy178III  
 SmlI  
 MnlI  
 MaeIII  
 Tsp45I  
 TATCGGAAGAGCAGGGATCTTTTATGCCTTCTCTCCAAATCTTGAGGTCACAAGTAACCT  
 2761 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2820  
 ATAGCCTTCTCGTCCCTAGAAAATACGGAAGAGAGGTTTAGAACTCCAGTGTTTCATTGGA  
 DpnI  
 BstYI  
 Sau3AI  
 MboII  
 ApoI  
 Tsp509I  
 BslI  
 Bcc83I  
 AluI  
 CviJI  
 Fnu4HI  
 TseI  
 AlwI  
 DpnI  
 MnlI  
 BglII  
 BstYI  
 Sau3AI  
 BbvI  
 CviRI  
 BsrI  
 ATCTATGGAATTTCGTGGATCTTCACGAGCTACAATGCAGATCTTGAGGTAAGTTCCA  
 2821 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2880  
 TAGATACCTTTAAGCACCTAGAAGTGCCTCGATGTTACGTCTAGAACCTCCATTCAAGGT  
 DdeI  
 Hpy178III

```

                                DpnI
                                BstYI
                                Sau3AI
                                BseMII
                                DpnI
                                Sau3AI
                                ApoI
                                Tsp509I
                                AlwI
                                DdeI
                                DdeI
                                BfaI
                                BsmFI
                                TTCTCAAAGA
2881 -----+----- 2940
CAAGATTTTCGCAAGGACTAGGGAATCTTTAAGATTCTCTAGGACTCACATAGATCCCTG

```

Enzymes that do cut:

AccI	AceIII	AciI	AclI	AflIII	AloI	AluI	AlwI
AlwNI	ApoI	AvaI	AvaII	BamHI	BanI	BanII	BbsI
BbvI	BbvCI	BccI	Bce83I	BcefI	BciVI	BfaI	BglII
BmgI	BmrI	BplI	BpmI	Bpu10I	BsaI	BsaBI	BsaHI
BsaJI	BsaXI	BsbI	BscGI	BseMII	BseRI	BseSI	BsgI
BsiHKAI	BslI	BsmI	BsmAI	BsmBI	BsmFI	Bsp1286I	BspGI
BspMI	BsrI	BsrGI	BssSI	BstAPI	BstDSI	BstYI	Bsu36I
BtsI	Cac8I	CjeI	CjePI	Clai	CviJI	CviRI	DdeI
DpnI	DraI	DrdII	EaeI	EarI	EciI	EcoO109I	EcoRII
FauI	Fnu4HI	FokI	HaeI	HaeII	HaeIII	HaeIV	HgaI
HhaI	Hin4I	HindIII	HinfI	HphI	Hpy178III	Hpy188IX	MaeII
MaeIII	MboII	MluI	MmeI	MnlI	MscI	MseI	MslI
MspI	MspAI	MunI	MwoI	NarI	NciI	NheI	NlaIII
NlaIV	PacI	Pfl1108I	PleI	PpiI	Psp5II	PstI	PvuII
RsaI	SacI	SacII	SapI	Sau96I	Sau3AI	ScrFI	SfaNI
SfcI	SimI	SmlI	SpeI	Sse8647I	SspI	Sth132I	StyI
TaaI	TaqI	TaqII	TatI	TauI	TfiI	ThaI	TseI
Tsp45I	Tsp509I	TspRI	Tth111I	Tth111II	XhoI	XmnI	

Enzymes that do not cut:

AarI	AatII	AflII	AhdI	ApaI	ApaLI	AscI	AvrII
BaeI	BcgI	BclI	BglI	Bpu1102I	BsaAI	BsaWI	BsiEI
Bsp24I	BspEI	BspLU11I	BsrBI	BsrDI	BsrFI	BssHII	BstEII
BstXI	BstZ17I	DraIII	DrdI	EagI	Eco47III	Eco57I	EcoNI
EcoRI	EcoRV	FseI	FspI	GdiII	HgiEII	HincII	HpaI
KpnI	NcoI	NdeI	NgoAIV	NotI	NruI	NsiI	NspI
NspV	PflMI	PinAI	PmeI	PmlI	PshAI	PvuI	RcaI
RleAI	RsrII	SalI	SanDI	SbfI	ScaI	SexAI	SfiI
SgfI	SgrAI	SmaI	SnaBI	SphI	Srfl	StuI	SunI
SwaI	VspI	XbaI	XcmI				



**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application No.: 09/857,128

Applicant: MURDIN, Andrew D. et al.

Filed: September 20, 2001

TC/A.U.: 1645

Examiner: Nita M. Minnifield

Docket No: 032931/0252

**DECLARATION OF ANDREW D. MURDIN  
PURSUANT TO 37 C.F.R. §1.132**

1. I, Andrew D. Murdin, Ph.D., am one of the named inventors of the above-identified patent application and am familiar with the contents and prosecution thereof.

2. Details of my employment history are as follows:

Since 2002	Director, External R&D Canada, Aventis Pasteur.
1999-2002	Principal Research Scientist, Aventis Pasteur.
1997-2002	Section Head, Aventis Pasteur.
1993-2003	Project Leader (Chlamydia), Aventis Pasteur.
1990-1993	Research Scientist, Connaught Laboratories Ltd. (subsequently Pasteur Merieux Connaught, subsequently Aventis Pasteur), Toronto, Canada.
1988-1990	Post-Doctoral Research Associate, Dept. of Microbiology, State University of New York, Stony Brook, NY, USA.
1985-1987	Post-Doctoral Research Fellow, Dept. of Microbiology, University of Surrey, Guildford, Surrey, England.
1981-1985	Scientific Officer, Vaccine Research Dept., Animal Virus Research Institute, Pirbright, Surrey, England.

Details of my education are as follows:

B.Sc., University of Bath, England, 1980

Ph.D., University of Surrey, England, 1986.

3. I am employed by Aventis Pasteur Limited, the assignee of the above-identified application. Between 1993 and 2003, I was responsible for the research project from which the above-identified patent application arose.
4. The experiment described below was carried out at Aventis Pasteur.
5. It has been previously demonstrated (Yang *et al.* Infect. Immun. May 1993. 61(5):2037-40) that mice are susceptible to intranasal infection with different isolates of *C. pneumoniae*. Strain AR-39 (Grayston *et al* (1990) Journal of Infectious Diseases 161:618-625) was used in Balb/c mice as a challenge infection model to examine the capacity of Chlamydia gene products delivered as naked DNA to elicit a protective response against a sublethal *C. pneumoniae* lung infection. Protective immunity is defined as an accelerated clearance of pulmonary infection.
6. Groups of 7 to 9 week old male Balb/c mice (8 to 10 per group) were immunized intramuscularly (i.m.) plus intranasally (i.n.) with plasmid DNA containing a sequence encoding the *C. pneumoniae* 98 kDa protein designated CPN100638 (plasmid pCAI638). Saline or the plasmid vector lacking an inserted Chlamydial gene was given to groups of control animals.
7. The sequence encoding the *C. pneumoniae* 98 kDa protein designated CPN100638 in plasmid pCAI638 is the same as SEQ ID No:6 (encoding SEQ ID No:14) of the above-identified patent application. Plasmid pCAI638 is based on plasmid pcDNA3.1(-)Myc-His C (Invitrogen), in which SEQ ID No:6 under control of the cytomegalovirus (CMV) promoter, was inserted.
8. For i.m. immunization, alternate left and right quadriceps of mice were injected with 100µg of DNA in 50µl of PBS on three occasions at 0, 3 and 6 weeks. For i.n. immunization, anaesthetized mice were aspirated 50µl of PBS containing 50 µg DNA on three occasions at 0, 3 and 6 weeks. At week 8, immunized mice were inoculated i.n.

with  $5 \times 10^5$  IFU of *C. pneumoniae*, strain AR39 in 100 $\mu$ l of SPG buffer to test their ability to limit the growth of a sublethal *C. pneumoniae* challenge.

9. Lungs were taken from mice at day 9 post-challenge and immediately homogenised in SPG buffer (7.5% sucrose, 5mM glutamate, 12.5mM phosphate pH7.5). The homogenate was stored frozen at  $-70^{\circ}\text{C}$  until assay. Dilutions of the homogenate were assayed for the presence of infectious Chlamydia by inoculation onto monolayers of susceptible cells. The inoculum was centrifuged onto the cells at 3000rpm for 1 hour, then the cells were incubated for three days at  $35^{\circ}\text{C}$  in the presence of 1 $\mu\text{g/ml}$  cycloheximide. After incubation the monolayers were fixed with formalin and methanol then immunoperoxidase stained for the presence of Chlamydial inclusions using convalescent sera from rabbits infected with *C. pneumoniae* and metal-enhanced DAB as a peroxidase substrate.

10. The attached Figure shows that mice immunized i.n. and i.m. with pCA1638 had Chlamydial lung titers less than 60,000 in 4 of 6 cases at day 9 (mean 85,483). The range of values for control mice sham immunized with saline was 85,000-250,000 IFU/lung (mean 166,288) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM1061, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice. The construct pCACPNM1061 is identical to pC1638 except that the nucleotide sequence encoding the 98 kDa protein is replaced with a *C. pneumoniae* nucleotide sequence encoding a Zinc Metalloprotease protein.


11. The above-described experiment illustrates that immunization of mice with an expression plasmid containing a nucleotide sequence encoding SEQ ID No:14, protects the mice against an intranasal challenge of *C. pneumoniae*.

12. I hereby declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like

are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.

4<sup>th</sup> March 2004

Date

A handwritten signature in black ink, appearing to read 'A. Murdin', with a long horizontal flourish extending to the right.

Andrew Murdin

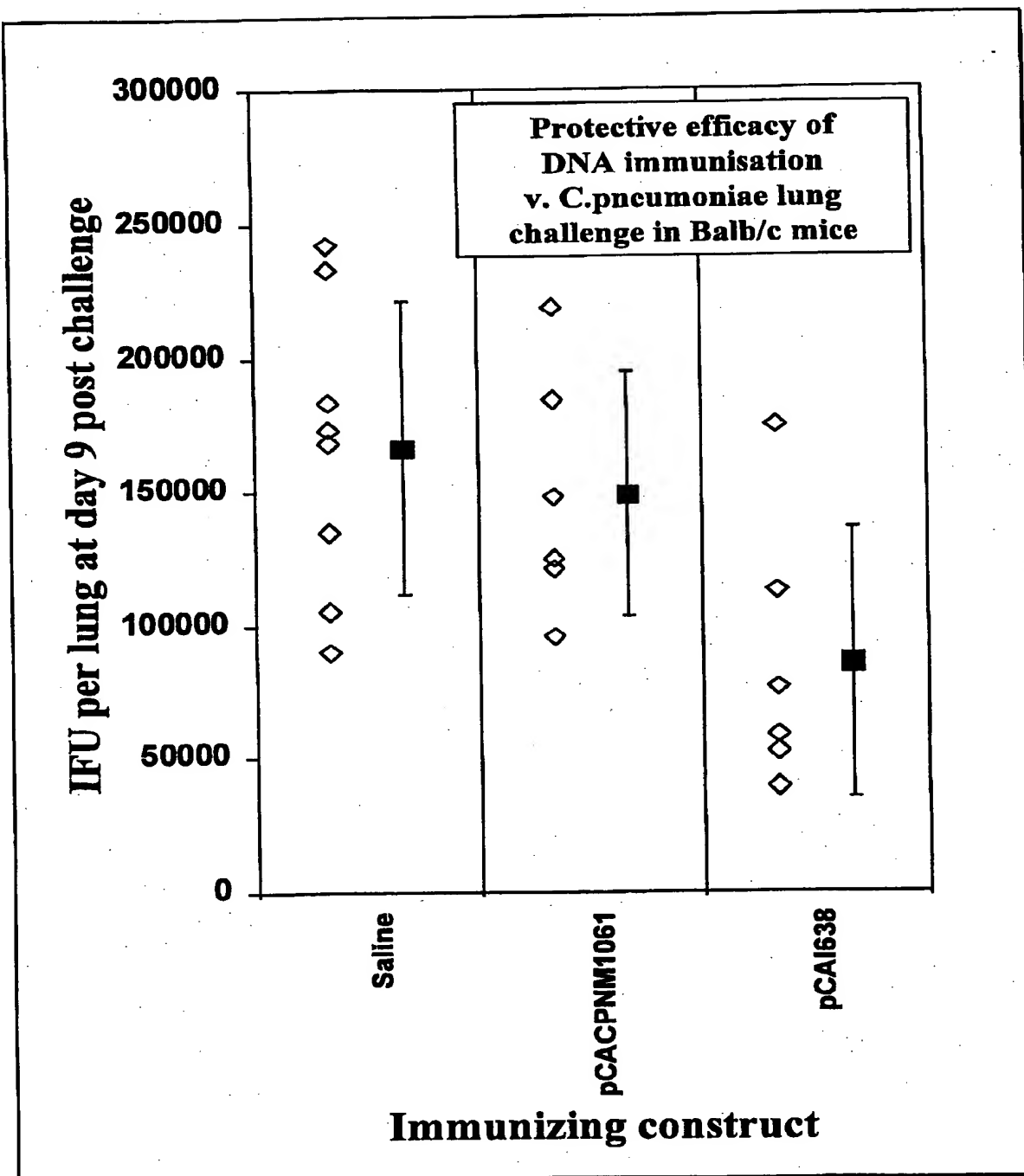


Fig 2

REPLACEMENT SHEET  
Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF

Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128

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Figure 1A: Nucleotide and deduced amino acid sequence of CPN100634

gataaaaatt cttgacagct gttttgtcat ctttaacttg atttacttat tttgtttcta															60
tattgatgcg aatagttctc taaaaaaca aagcattacc atg aag act tcg att															115
															Met Lys Thr Ser Ile
															1 5
cct tgg gtt tta gtt tcc tcc gtg tta gct ttc tca tgt cac cta cag															163
Pro Trp Val Leu Val Ser Ser Val Leu Ala Phe Ser Cys His Leu Gln															
															10 15 20
tca cta gct aac gag gaa ctt tta tca cct gat gat agc ttt aat gga															211
Ser Leu Ala Asn Glu Glu Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly															
															25 30 35
aat atc gat tca gga acg ttt act cca aaa act tca gcc aca aca tat															259
Asn Ile Asp Ser Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr															
															40 45 50
tct cta aca gga gat gtc ttc ttt tac gag cct gga aaa ggc act ccc															307
Ser Leu Thr Gly Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro															
															55 60 65
tta tct gac agt tgt ttt aag caa acc acg gac aat ctt acc ttc ttg															355
Leu Ser Asp Ser Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu															
															70 75 80 85
ggg aac ggt cat agc tta acg ttt ggc ttt ata gat gct ggc act cat															403
Gly Asn Gly His Ser Leu Thr Phe Gly Phe Ile Asp Ala Gly Thr His															
															90 95 100
gca ggt gct gct gca tct aca aca gca aat aag aat ctt acc ttc tca															451
Ala Gly Ala Ala Ala Ser Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser															
															105 110 115
ggg ttt tcc tta ctg agt ttt gat tcc tct cct agc aca acg gtt act															499
Gly Phe Ser Leu Leu Ser Phe Asp Ser Ser Pro Ser Thr Thr Val Thr															
															120 125 130
aca ggt cag gga acg ctt tcc tca gca gga ggc gta aat tta gaa aat															547
Thr Gly Gln Gly Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn															
															135 140 145
att cgt aaa ctt gta gtt gct ggg aat ttt tct act gca gat ggt gga															595
Ile Arg Lys Leu Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly															
															150 155 160 165
gct atc aaa gga gcg tct ttc ctt tta act ggc act tct gga gat gct															643
Ala Ile Lys Gly Ala Ser Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala															
															170 175 180
ctt ttt agt aac aac tct tca tca aca aag gga gga gca att gct act															691
Leu Phe Ser Asn Asn Ser Ser Ser Thr Lys Gly Gly Ala Ile Ala Thr															
															185 190 195



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Thr Ala Gly Ala Arg Ile Ala Asn Asn Thr Gly Tyr Val Arg Phe Leu	
200 205 210	
tct aac ata gcg tct acg tca gga ggc gct atc gat gat gaa ggc acg	787
Ser Asn Ile Ala Ser Thr Ser Gly Gly Ala Ile Asp Asp Glu Gly Thr	
215 220 225	
tcg ata cta tcg aac aac aaa ttt cta tat ttt gaa ggg aat gca gcg	835
Ser Ile Leu Ser Asn Asn Lys Phe Leu Tyr Phe Glu Gly Asn Ala Ala	
230 235 240 245	
aaa act act ggc ggt gcg atc tgc aac acc aag gcg agt gga tct cct	883
Lys Thr Thr Gly Gly Ala Ile Cys Asn Thr Lys Ala Ser Gly Ser Pro	
250 255 260	
gaa ctg ata atc tct aac aat aag act ctg atc ttt gct tca aac gta	931
Glu Leu Ile Ile Ser Asn Asn Lys Thr Leu Ile Phe Ala Ser Asn Val	
265 270 275	
gca gaa aca agc ggt ggc gcc atc cat gct aaa aag cta gcc ctt tcc	979
Ala Glu Thr Ser Gly Gly Ala Ile His Ala Lys Lys Leu Ala Leu Ser	
280 285 290	
tct gga ggc ttt aca gag ttt cta cga aat aat gtc tca tca gca act	1027
Ser Gly Gly Phe Thr Glu Phe Leu Arg Asn Asn Val Ser Ser Ala Thr	
295 300 305	
cct aag ggg ggt gct atc agc atc gat gcc tca gga gag ctc agt ctt	1075
Pro Lys Gly Gly Ala Ile Ser Ile Asp Ala Ser Gly Glu Leu Ser Leu	
310 315 320 325	
tct gca gag aca gga aac att acc ttt gta aga aat acc ctt aca aca	1123
Ser Ala Glu Thr Gly Asn Ile Thr Phe Val Arg Asn Thr Leu Thr Thr	
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acc gga agt acc gat act cct aaa cgt aat gcg atc aac ata gga agt	1171
Thr Gly Ser Thr Asp Thr Pro Lys Arg Asn Ala Ile Asn Ile Gly Ser	
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aac ggg aaa ttc acg gaa tta cgg gct gct aaa aat cat aca att ttc	1219
Asn Gly Lys Phe Thr Glu Leu Arg Ala Ala Lys Asn His Thr Ile Phe	
360 365 370	
ttc tat gat ccc atc act tca gaa gga acc tca tca gac gta ttg aag	1267
Phe Tyr Asp Pro Ile Thr Ser Glu Gly Thr Ser Ser Asp Val Leu Lys	
375 380 385	
ata aat aac ggc tct gcg gga gct ctc aat cca tat caa gga acg att	1315
Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro Tyr Gln Gly Thr Ile	
390 395 400 405	
cta ttt tct gga gaa acc cta aca gca gat gaa ctt aaa gtt gct gac	1363
Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu Leu Lys Val Ala Asp	
410 415 420	



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425 430 435

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570 575 580

gag gcc acg gca act tgg acc aaa aca gga ttt gtt ccc agc ccc gaa 1891  
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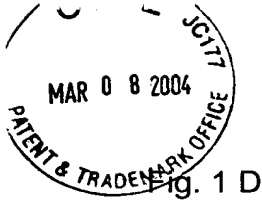


Fig. 1 D

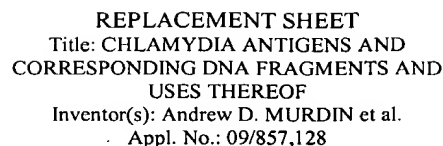
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gtc atc ggt gga agt gct cac act cct aaa gac gac cta ttt acc ttt	2131
Val Ile Gly Gly Ser Ala His Thr Pro Lys Asp Asp Leu Phe Thr Phe	
665 670 675	
gcg ttc tgc cat ctc ttt gct aga gac aaa gat tgt ttt atc gct cac	2179
Ala Phe Cys His Leu Phe Ala Arg Asp Lys Asp Cys Phe Ile Ala His	
680 685 690	
aac aac tct aga acc tac ggt gga act tta ttc ttc aag cac tct cat	2227
Asn Asn Ser Arg Thr Tyr Gly Gly Thr Leu Phe Phe Lys His Ser His	
695 700 705	
acc cta caa ccc caa aac tat ttg aga tta gga aga gca aag ttt tct	2275
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710 715 720 725	
gaa tca gct ata gaa aaa ttc cct agg gaa att ccc cta gcc ttg gat	2323
Glu Ser Ala Ile Glu Lys Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp	
730 735 740	
gtc caa gtt tcg ttc agc cat tca gac aac cgt atg gaa acg cac tat	2371
Val Gln Val Ser Phe Ser His Ser Asp Asn Arg Met Glu Thr His Tyr	
745 750 755	
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760 765 770	
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Gly Gly Ile Gly Leu Asp Leu Pro Phe Val Leu Ser Asn Pro His Pro	
775 780 785	
ctt ttc aag acc ttc att cca cag atg aaa gtc gaa atg gtt tat gta	2515
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Ile Gly Arg Leu Leu Asn Leu Ser Ile Pro Val Gly Ala Lys Phe Val	
825 830 835	
cag ggg gat atc gga gat tcc tac acc tat gat ctc tca gga ttc ttt	2659
Gln Gly Asp Ile Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe	
840 845 850	
gtt tcc gat gtc tat cgt aac aat ccc caa tct aca gcg act ctt gtg	2707
Val Ser Asp Val Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val	
855 860 865	

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Fig. 1 E

atg agc cca gac tct tgg aaa att cgc ggt ggc aat ctt tca aga cag	2755
Met Ser Pro Asp Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln	
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gca ttt tta ctg agg ggt agc aac aac tac gtc tac aac tcc aat tgt	2803
Ala Phe Leu Leu Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys	
890 895 900	
gag ctc ttc gga cat tac gct atg gaa ctc cgt gga tct tca agg aac	2851
Glu Leu Phe Gly His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn	
905 910 915	
tac aat gta gat gtt ggt acc aaa ctc cga ttc tagattgcta aaactcccta	2904
Tyr Asn Val Asp Val Gly Thr Lys Leu Arg Phe	
920 925	
gttcttctag ggagttttct catactttta gggaaatatt tgctat	2950





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Fig. 2 B

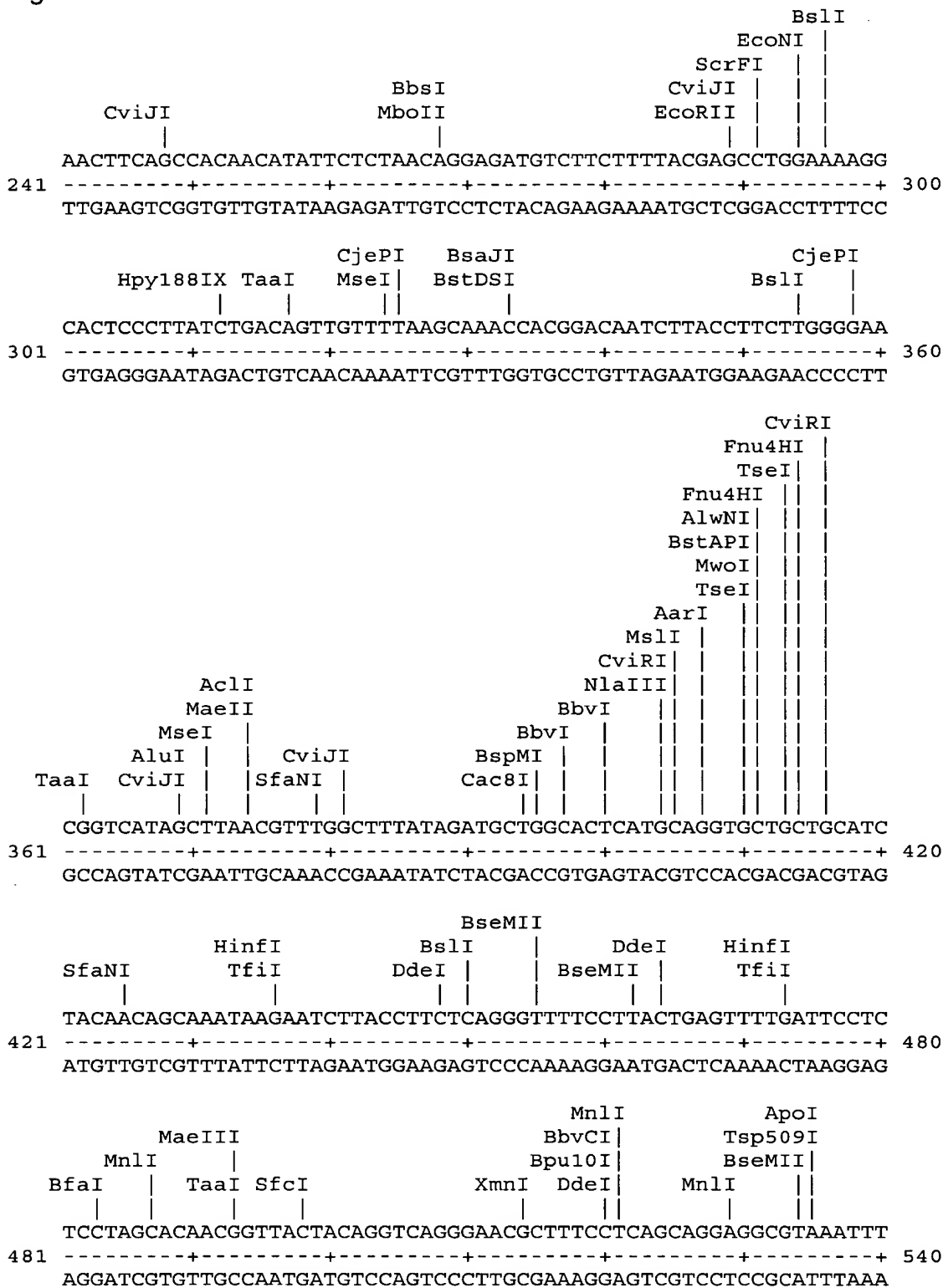




Fig. 2 C

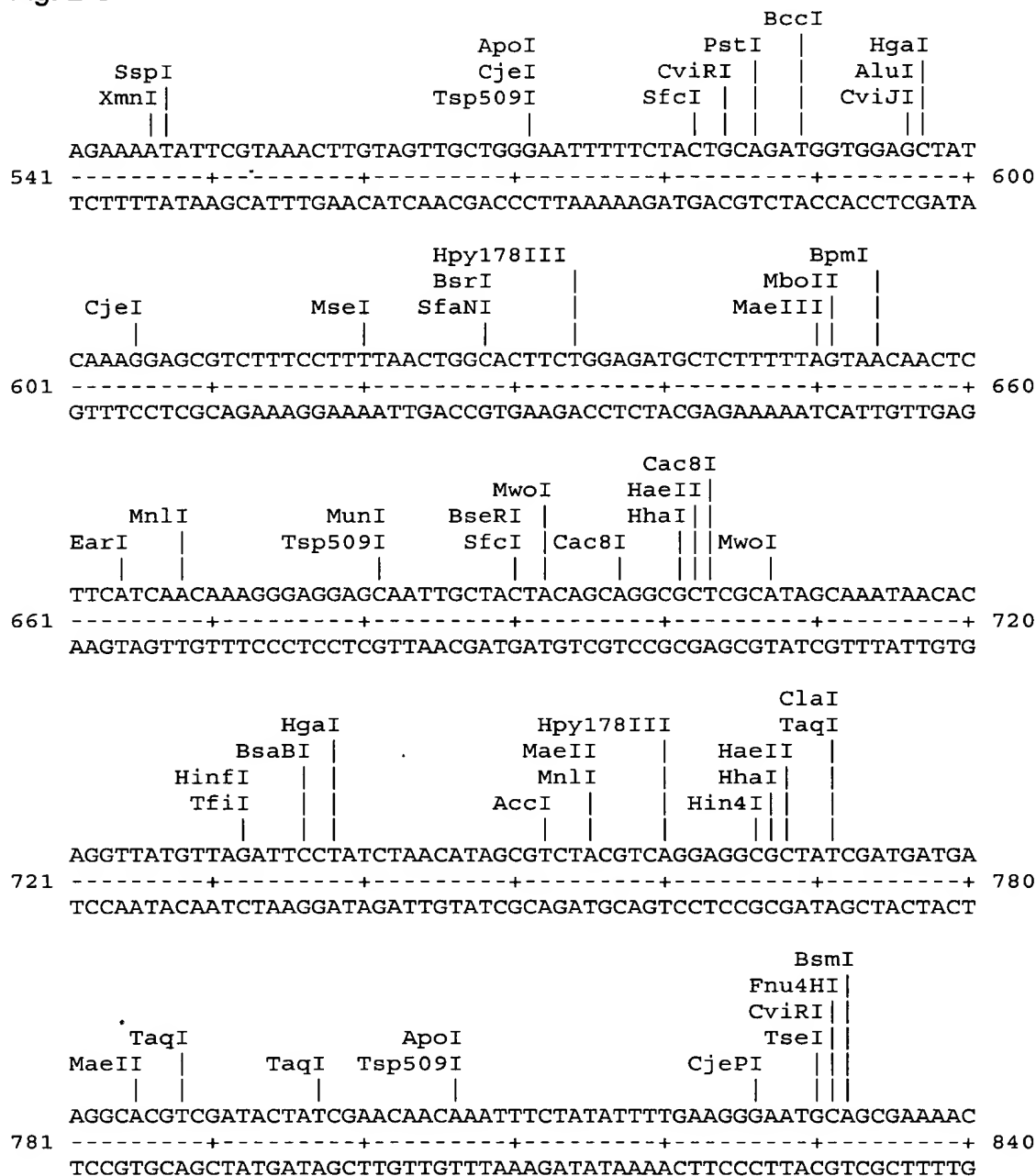
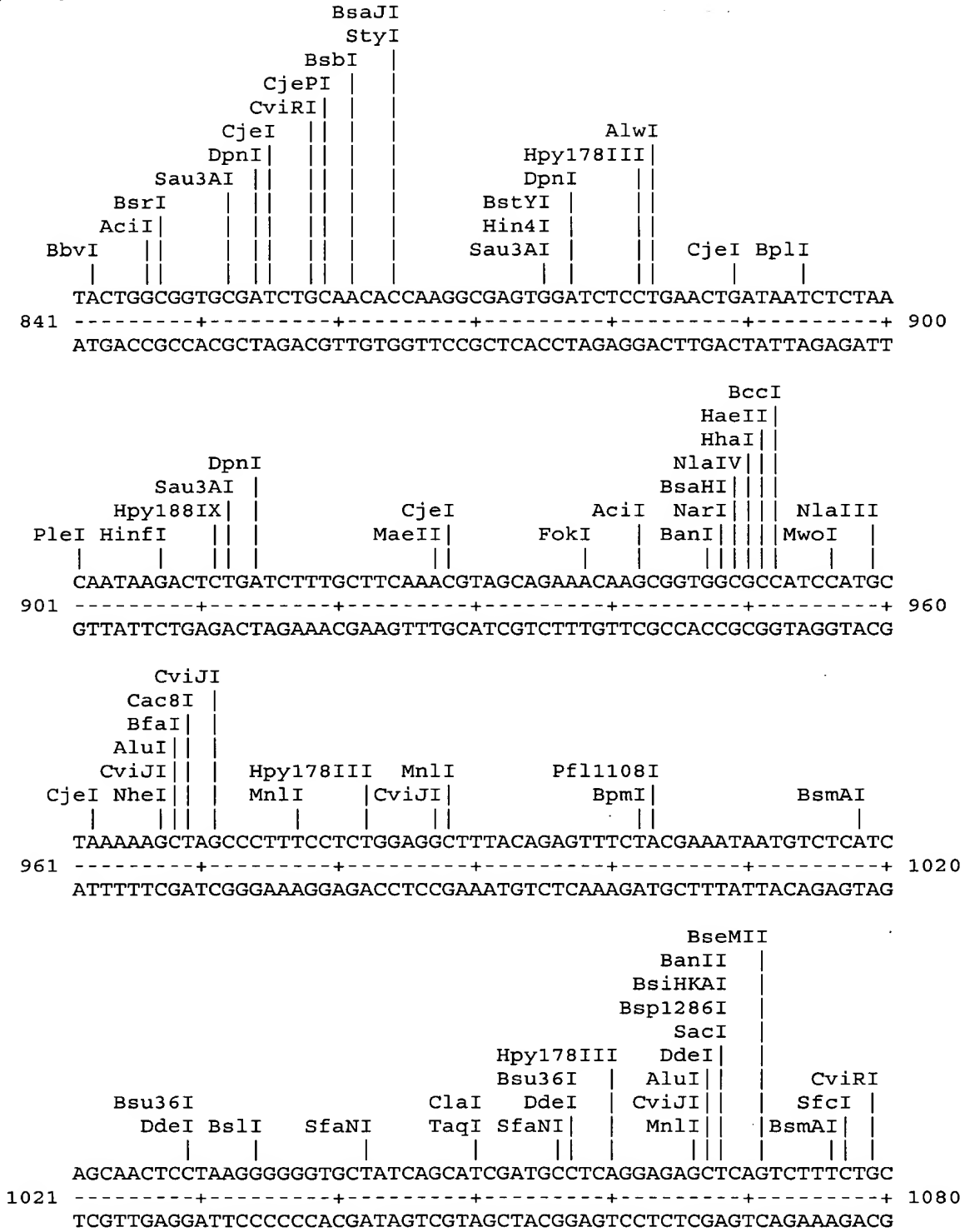


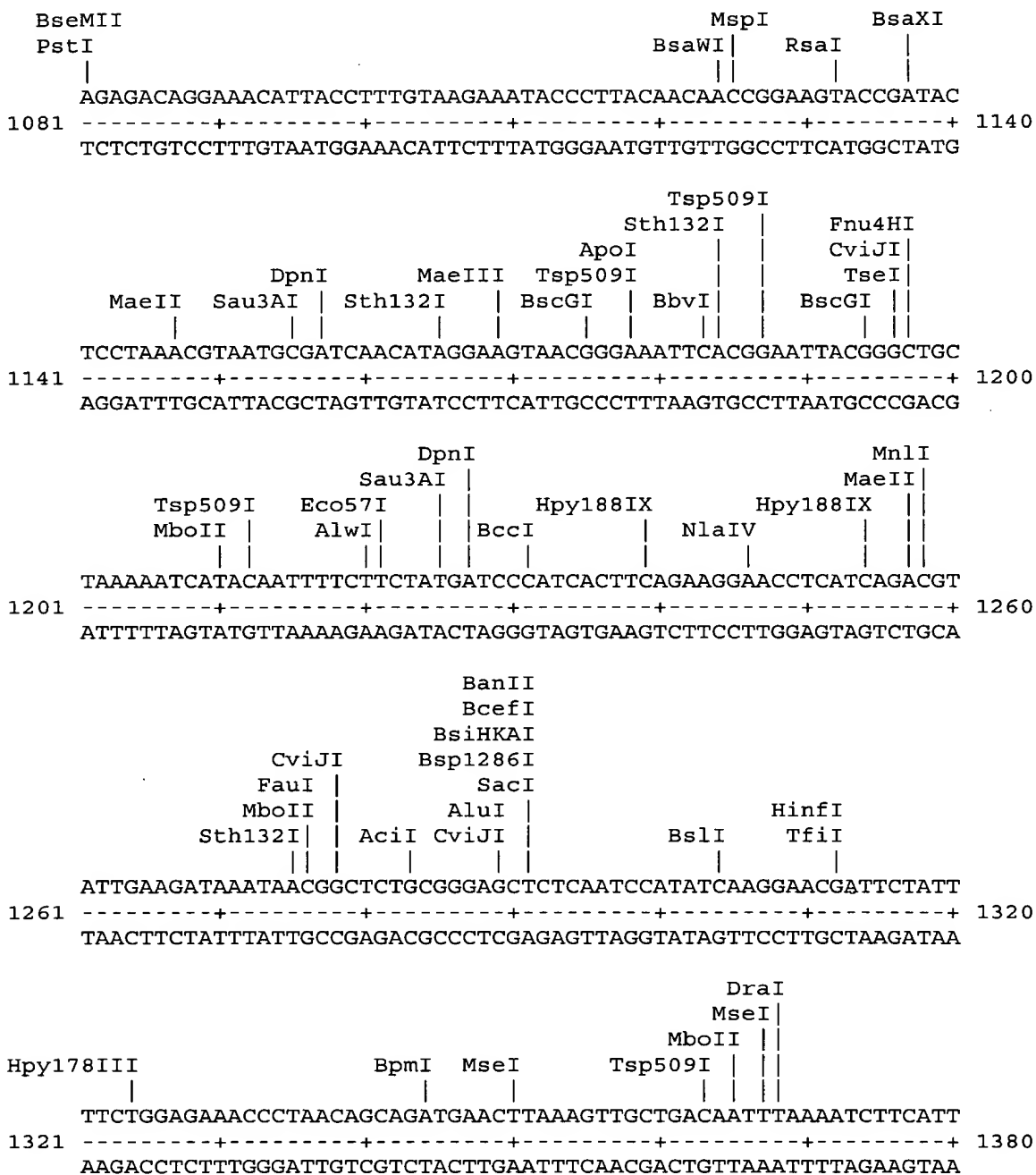


Fig. 2 D



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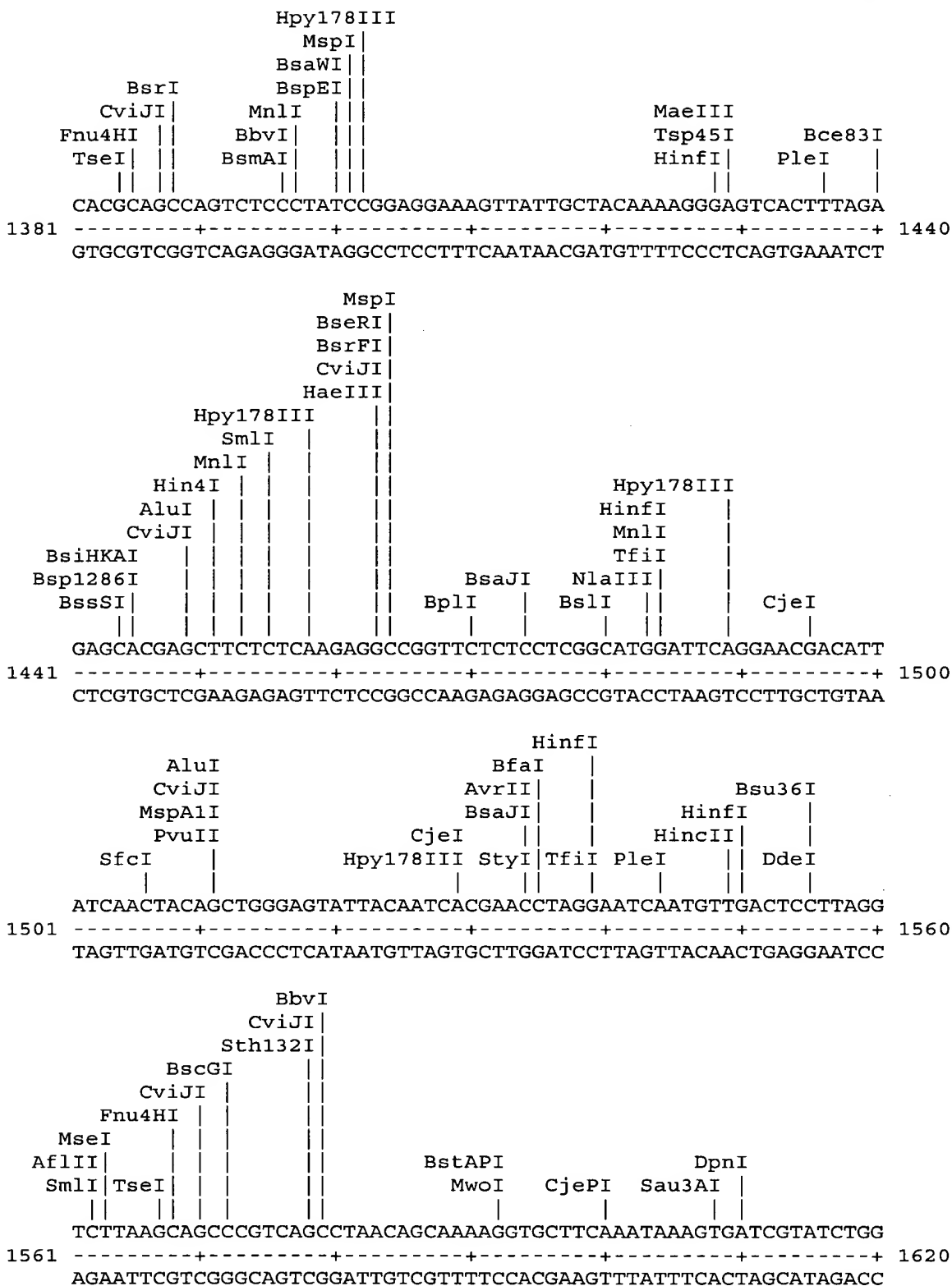
Fig. 2 E





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Fig. 2 F





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Fig. 2 G

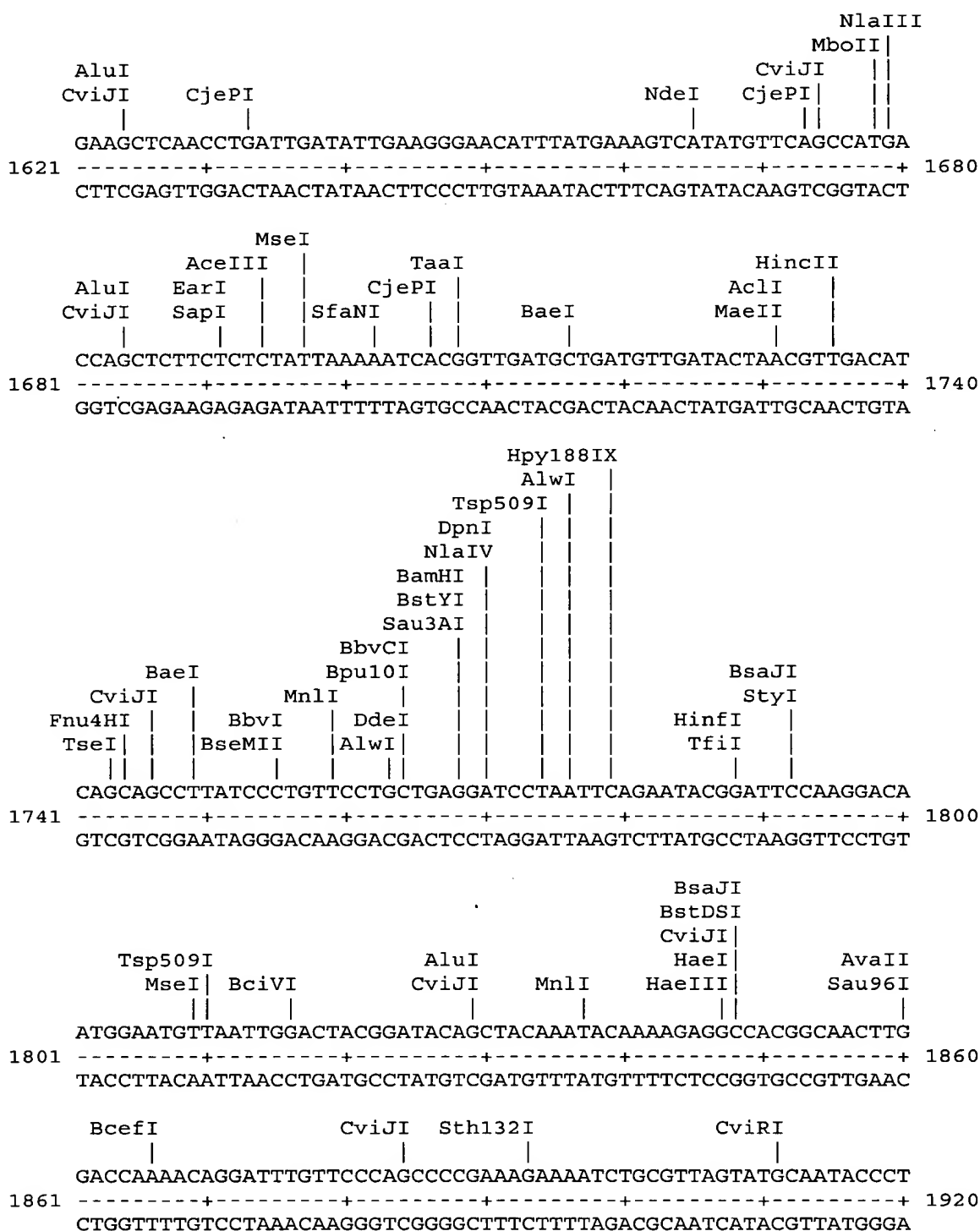




Fig. 2 I

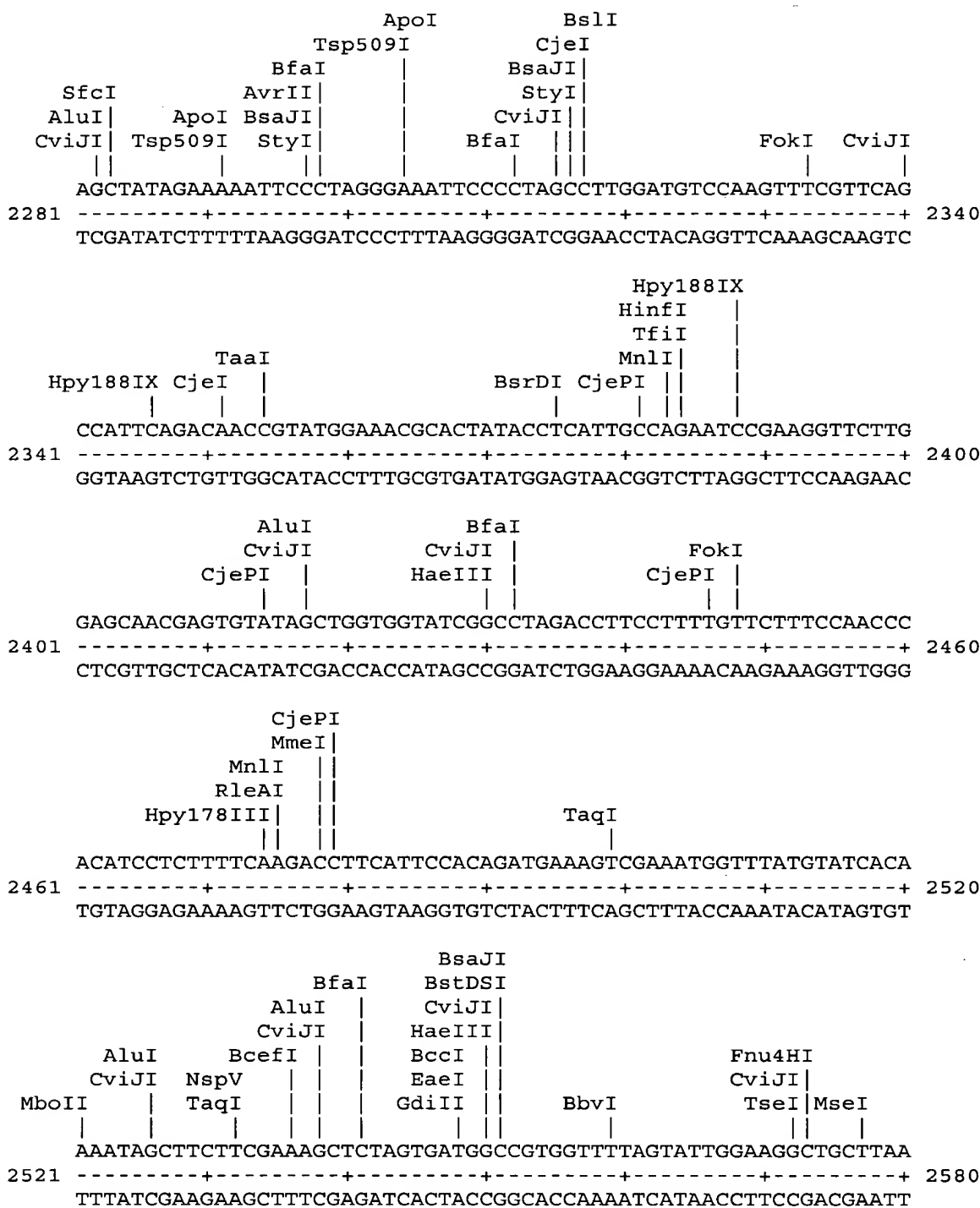
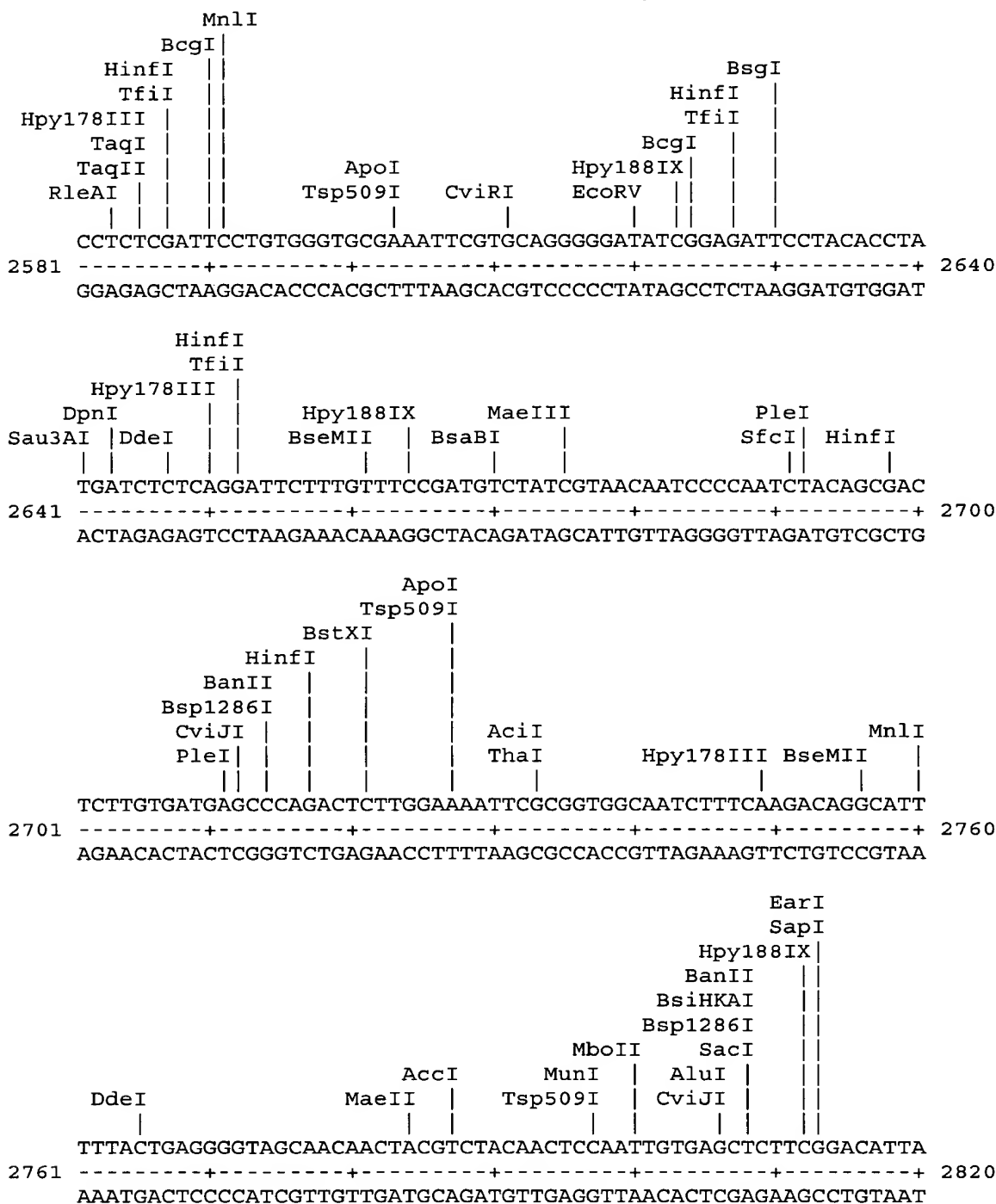


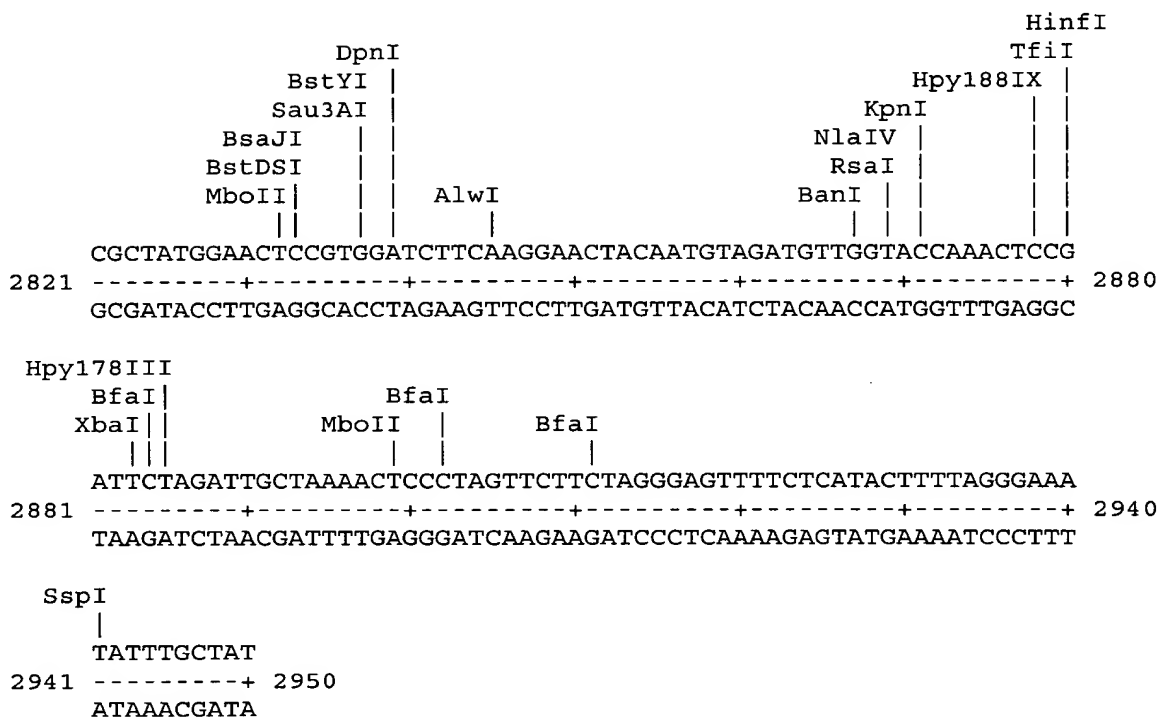
Fig. 2 J





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Fig. 2 K





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Figure 3 A: Nucleotide and deduced amino acid sequence of CPN100635

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                                     Met Lys Ser Gln Phe
                                     1 5
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Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys Phe Thr Ser Cys Ser
                                     10 15 20
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Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly Pro Ser Asp Ser Phe
                                     25 30 35
gac gga agt act aac aca ggc acc tat act cct aaa aat acg act act 259
Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro Lys Asn Thr Thr Thr
                                     40 45 50
gga ata gac tat act ctg aca gga gat ata act ctg caa aac ctt ggg 307
Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly
Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly
                                     55 60 65
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Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser Asp Thr Thr Glu Ser
                                     70 75 80 85
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                                     90 95 100
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Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr Thr Asp Lys Asn Leu
                                     105 110 115
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Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser
                                     120 125 130
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Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val Lys Cys Gly Gly Asp
                                     135 140 145
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Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys
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```



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Fig. 3 B

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Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn	
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Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly	
Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly	
185 190 195	
aaa aaa ggt ggg gct att tgt gct act ggt act gta gat att aca aat	739
Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn	
Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn	
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230 235 240 245	
ctt gta ttt tct gaa aat agt gtg aca gcg acc gca gga aat gga gga	883
Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly	
Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly	
250 255 260	
gct ctt tct gga gat gcc gat gtt acc ata tct ggg aat cag agt gta	931
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Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser Gly Asn Gln Ser Val	
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Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly Gly Asn Pro Phe Ser	
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Ile Leu Ala Ala Gly Glu Cys Ser Leu Phe Ser Glu Ala Gly Asp His	
330 335 340	



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Fig. 3 C

tac ctt aat ggg aat gcc att gtt gca act aca cca caa act aca aaa	1171
Tyr Leu Asn Gly Asn Ala Ile Val Ala Thr Thr Pro Gln Thr Thr Lys	
Tyr Leu Asn Gly Asn Ala Ile Val Ala Thr Thr Pro Gln Thr Thr Lys	
345 350 355	
aga aat tct att gac ata gga tct act ggc aaa gat cac gaa tta cgt	1219
Arg Asn Ser Ile Asp Ile Gly Ser Thr Gly Lys Asp His Glu Leu Arg	
Arg Asn Ser Ile Asp Ile Gly Ser Thr Gly Lys Asp His Glu Leu Arg	
360 365 370	
gca ata tct ggg cat agc atc ttt ttc tac gat ccg att act gct aat	1267
Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn	
Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn	
375 380 385	
acg gct gcg gat tct aca gat act tta aat ctc aat aag gct gat gca	1315
Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala	
Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala	
390 395 400 405	
ggg aat agt aca gat tat agt ggg tcg att gtt ttt tct ggt gaa aag	1363
Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val Phe Ser Gly Glu Lys	
Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val Phe Ser Gly Glu Lys	
410 415 420	
ctc tct gaa gat gaa gca aaa gtt gca gac aac ctc act tct acg ctg	1411
Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn Leu Thr Ser Thr Leu	
Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn Leu Thr Ser Thr Leu	
425 430 435	
aag cag cct gta act cta act gca gga aat tta gta ctt aaa cgt ggt	1459
Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu Val Leu Lys Arg Gly	
Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu Val Leu Lys Arg Gly	
440 445 450	
gtc act ctc gat acg aaa ggc ttt act cag acc gcg ggt tcc tct gtt	1507
Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr Ala Gly Ser Ser Val	
Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr Ala Gly Ser Ser Val	
455 460 465	
att atg gat gcg ggc aca acg tta aaa gca agt aca gag gag gtc act	1555
Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser Thr Glu Glu Val Thr	
Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser Thr Glu Glu Val Thr	
470 475 480 485	
tta aca ggt ctt tcc att cct gta gac tct tta ggc gag ggt aag aaa	1603
Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu Gly Glu Gly Lys Lys	
Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu Gly Glu Gly Lys Lys	
490 495 500	
gtt gta att gct gct tct gca gca agt aaa aat gta gcc ctt agt ggt	1651
Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn Val Ala Leu Ser Gly	
Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn Val Ala Leu Ser Gly	
505 510 515	





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Fig. 3 D

ccg att ctt ctt ttg gat aac caa ggg aat gct tat gaa aat cac gac	1699
Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala Tyr Glu Asn His Asp	
Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala Tyr Glu Asn His Asp	
520 525 530	
tta gga aaa act caa gac ttt tca ttt gtg cag ctc tct gct ctg ggt	1747
Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln Leu Ser Ala Leu Gly	
Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln Leu Ser Ala Leu Gly	
535 540 545	
act gca aca act aca gat gtt cca gcg gtt cct aca gta gca act cct	1795
Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro Thr Val Ala Thr Pro	
Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro Thr Val Ala Thr Pro	
550 555 560 565	
acg cac tat ggg tat caa ggt act tgg gga atg act tgg gtt gat gat	1843
Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met Thr Trp Val Asp Asp	
Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met Thr Trp Val Asp Asp	
570 575 580	
acc gca agc act cca aag act aag aca gcg aca tta gct tgg acc aat	1891
Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn	
Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn	
585 590 595	
aca ggc tac ctt ccg aat cct gag cgt caa gga cct tta gtt cct aat	1939
Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn	
Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn	
600 605 610	
agc ctt tgg gga tct ttt tca gac atc caa gcg att caa ggt gtc ata	1987
Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala Ile Gln Gly Val Ile	
Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala Ile Gln Gly Val Ile	
615 620 625	
gag aga agt gct ttg act ctt tgt tca gat cga ggc ttc tgg gct gcg	2035
Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala	
Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala	
630 635 640 645	
gga gtc gcc aat ttc tta gat aaa gat aag aaa ggg gaa aaa cgc aaa	2083
Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys	
Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys	
650 655 660	
tac cgt cat aaa tct ggt gga tat gct atc gga ggt gca gcg caa act	2131
Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr	
Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr	
665 670 675	
tgt tct gaa aac tta att agc ttt gcc ttt tgc caa ctc ttt ggt agc	2179
Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser	
Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser	
680 685 690	



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Fig. 3 E

gat	aaa	gat	ttc	tta	gtc	gct	aaa	aat	cat	act	gat	acc	tat	gca	gga	2227
Asp	Lys	Asp	Phe	Leu	Val	Ala	Lys	Asn	His	Thr	Asp	Thr	Tyr	Ala	Gly	
Asp	Lys	Asp	Phe	Leu	Val	Ala	Lys	Asn	His	Thr	Asp	Thr	Tyr	Ala	Gly	
	695						700				705					
gcc	ttc	tat	atc	caa	cac	att	aca	gaa	tgt	agt	ggg	ttc	ata	ggt	tgt	2275
Ala	Phe	Tyr	Ile	Gln	His	Ile	Thr	Glu	Cys	Ser	Gly	Phe	Ile	Gly	Cys	
Ala	Phe	Tyr	Ile	Gln	His	Ile	Thr	Glu	Cys	Ser	Gly	Phe	Ile	Gly	Cys	
	710					715				720					725	
ctc	tta	gat	aaa	ctt	cct	ggc	tct	tgg	agt	cat	aaa	ccc	ctc	gtt	tta	2323
Leu	Leu	Asp	Lys	Leu	Pro	Gly	Ser	Trp	Ser	His	Lys	Pro	Leu	Val	Leu	
Leu	Leu	Asp	Lys	Leu	Pro	Gly	Ser	Trp	Ser	His	Lys	Pro	Leu	Val	Leu	
				730					735					740		
gaa	ggg	cag	ctc	gct	tat	agc	cac	gtc	agt	aat	gat	ctg	aag	aca	aag	2371
Glu	Gly	Gln	Leu	Ala	Tyr	Ser	His	Val	Ser	Asn	Asp	Leu	Lys	Thr	Lys	
Glu	Gly	Gln	Leu	Ala	Tyr	Ser	His	Val	Ser	Asn	Asp	Leu	Lys	Thr	Lys	
			745					750					755			
tat	act	gcg	tat	cct	gag	gtg	aaa	ggg	tct	tgg	ggg	aat	aat	gct	ttt	2419
Tyr	Thr	Ala	Tyr	Pro	Glu	Val	Lys	Gly	Ser	Trp	Gly	Asn	Asn	Ala	Phe	
Tyr	Thr	Ala	Tyr	Pro	Glu	Val	Lys	Gly	Ser	Trp	Gly	Asn	Asn	Ala	Phe	
			760					765						770		
aac	atg	atg	ttg	gga	gct	tct	tct	cat	tct	tat	cct	gaa	tac	ctg	cat	2467
Asn	Met	Met	Leu	Gly	Ala	Ser	Ser	His	Ser	Tyr	Pro	Glu	Tyr	Leu	His	
Asn	Met	Met	Leu	Gly	Ala	Ser	Ser	His	Ser	Tyr	Pro	Glu	Tyr	Leu	His	
	775					780					785					
tgt	ttt	gat	acc	tat	gct	cca	tac	atc	aaa	ctg	aat	ctg	acc	tat	ata	2515
Cys	Phe	Asp	Thr	Tyr	Ala	Pro	Tyr	Ile	Lys	Leu	Asn	Leu	Thr	Tyr	Ile	
Cys	Phe	Asp	Thr	Tyr	Ala	Pro	Tyr	Ile	Lys	Leu	Asn	Leu	Thr	Tyr	Ile	
	790					795				800					805	
cgt	cag	gac	agc	ttc	tcg	gag	aaa	ggg	aca	gaa	gga	aga	tct	ttt	gat	2563
Arg	Gln	Asp	Ser	Phe	Ser	Glu	Lys	Gly	Thr	Glu	Gly	Arg	Ser	Phe	Asp	
Arg	Gln	Asp	Ser	Phe	Ser	Glu	Lys	Gly	Thr	Glu	Gly	Arg	Ser	Phe	Asp	
				810					815					820		
gac	agc	aac	ctc	ttc	aat	tta	tct	ttg	cct	ata	ggg	gtg	aag	ttt	gag	2611
Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile	Gly	Val	Lys	Phe	Glu	
Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile	Gly	Val	Lys	Phe	Glu	
			825					830					835			
aag	ttc	tct	gat	tgt	aat	gac	ttt	tct	tat	gat	ctg	act	tta	tcc	tat	2659
Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp	Leu	Thr	Leu	Ser	Tyr	
Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp	Leu	Thr	Leu	Ser	Tyr	
			840					845				850				
gtt	cct	gat	ctt	atc	cgc	aat	gat	ccc	aaa	tgc	act	aca	gca	ctt	gta	2707
Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys	Thr	Thr	Ala	Leu	Val	
Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys	Thr	Thr	Ala	Leu	Val	
	855						860				865					



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Fig. 3 F

```
atc agc gga gcc tct tgg gaa act tat gcc aat aac tta gca cga cag 2755
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Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln
870 875 880 885

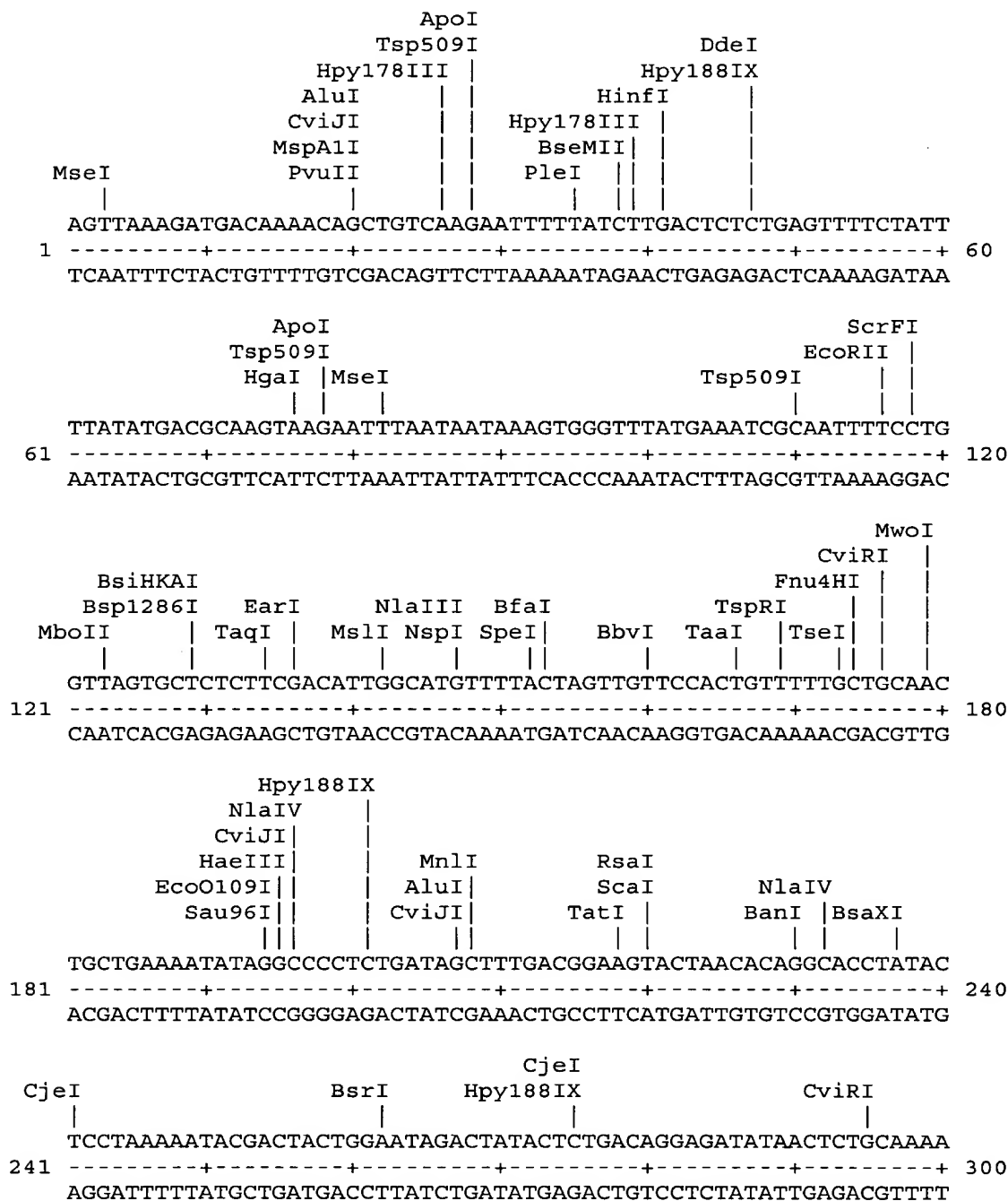
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Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala Phe Ser Pro Met Phe
890 895 900

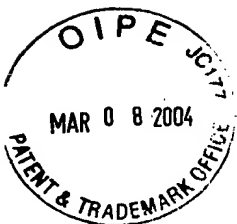
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Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg Gly Ser Ser Arg Ile
Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg Gly Ser Ser Arg Ile
905 910 915

tat aat gta gat ctt ggg ggt aag ttc caa ttc taggagcgtc tctcatgtct 2904
Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe
Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe
920 925

cagaaattct gagagagatc gcatttagga ttttcttaaa cacgac 2950
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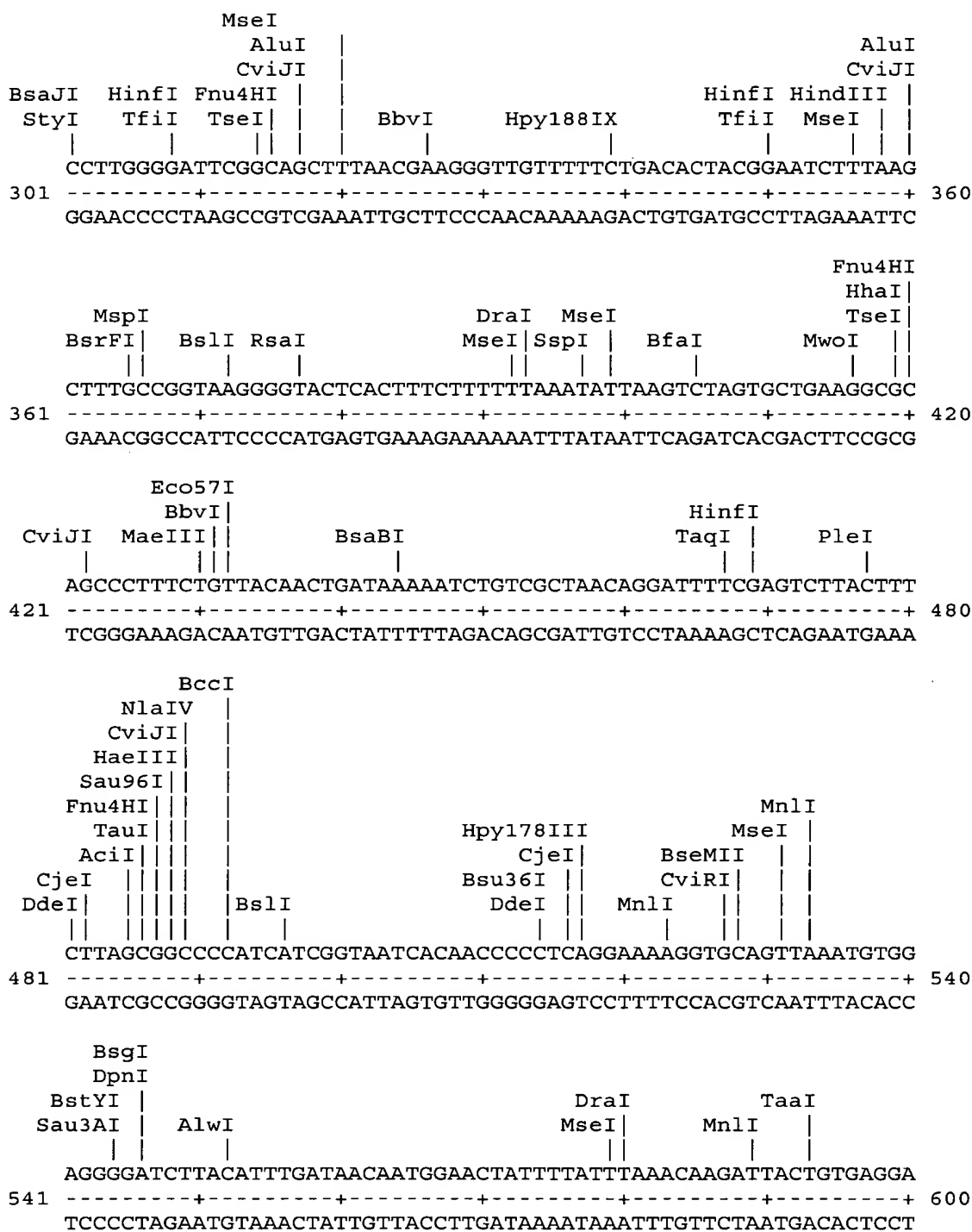
**Figure 4 A: Restriction enzyme analysis of CPN100635**





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Fig. 4 B



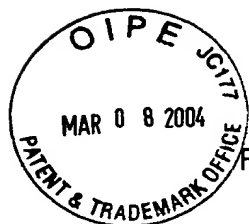
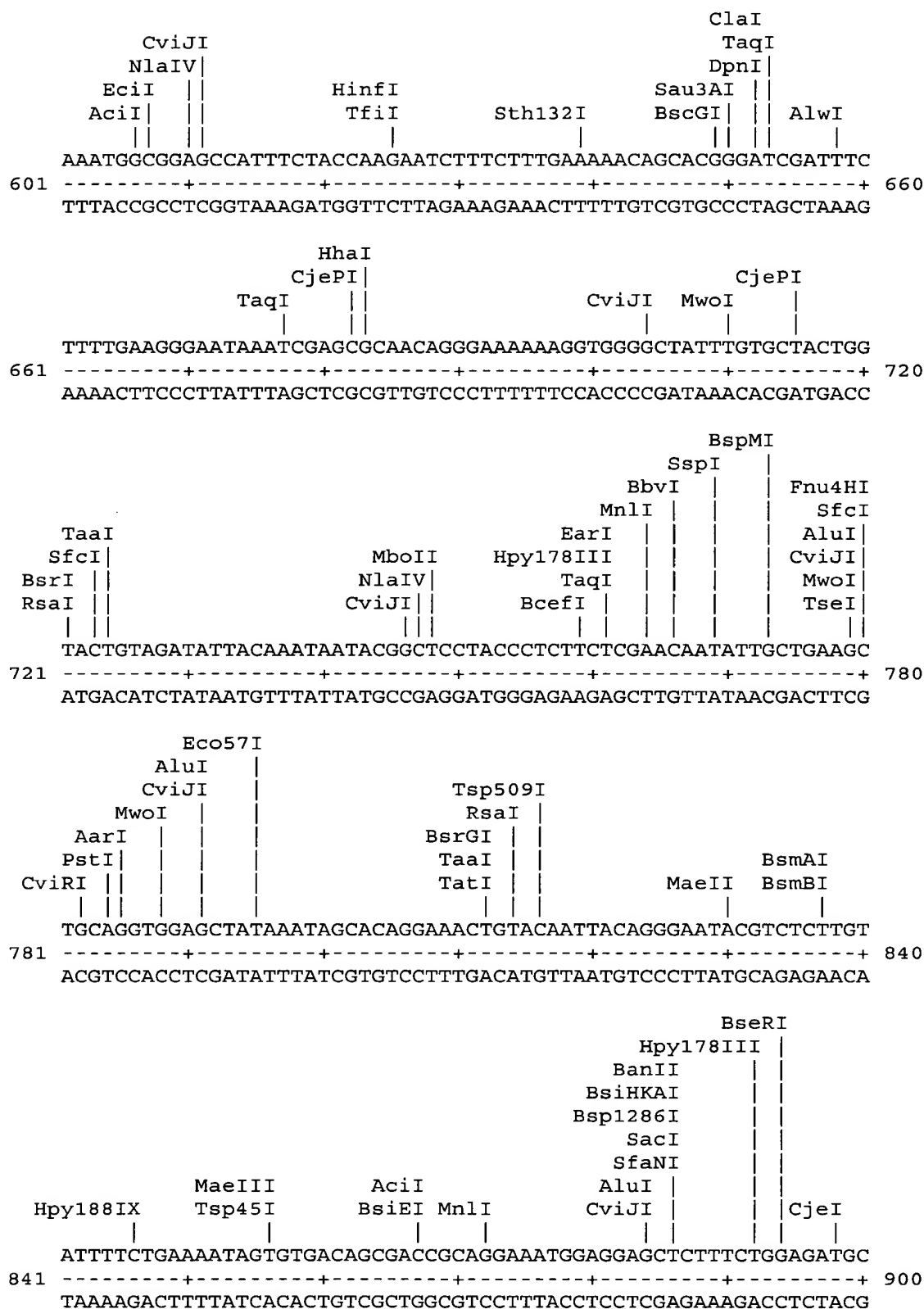


Fig. 4 C

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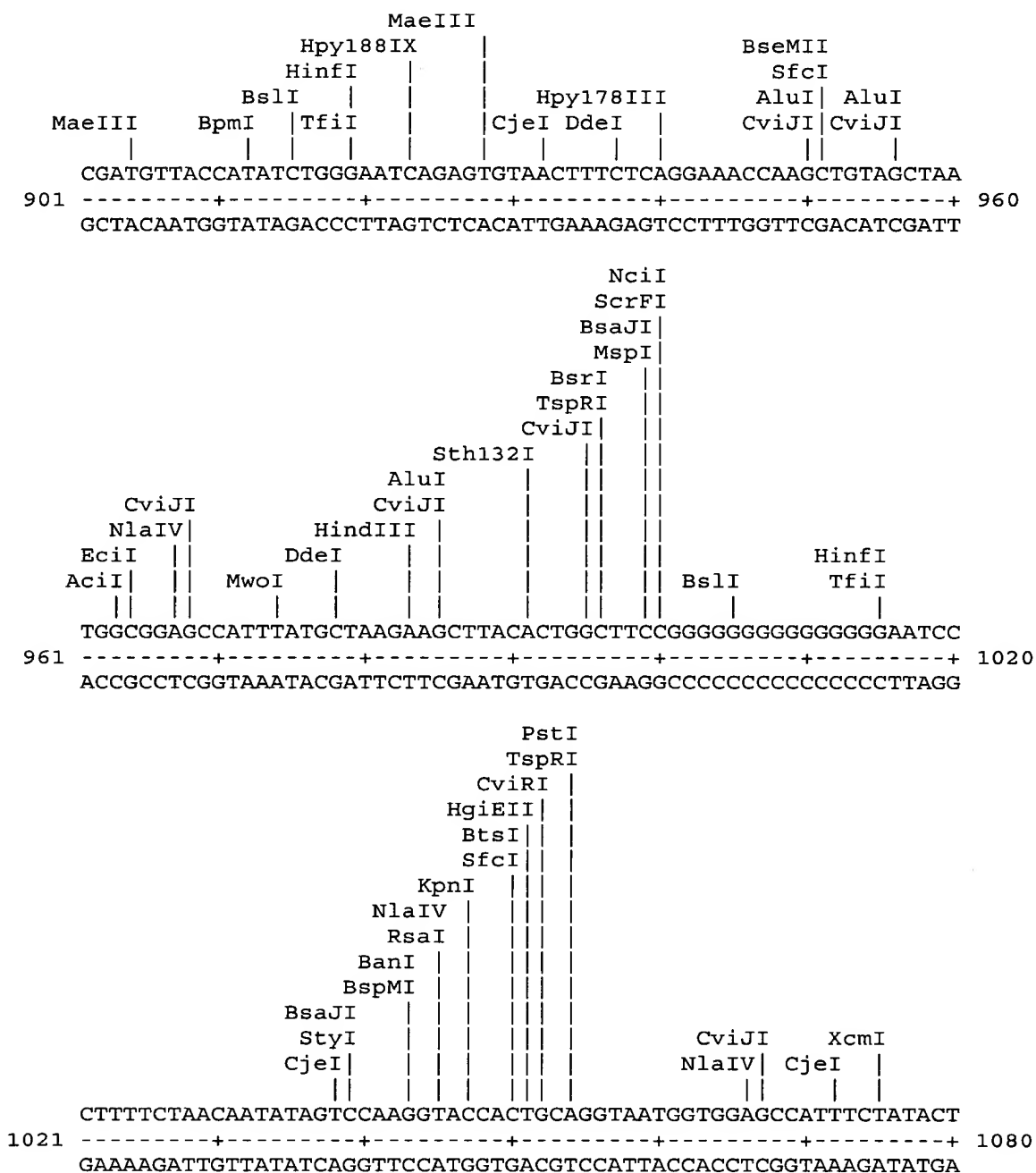
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CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128

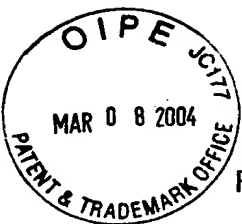




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Fig. 4 D





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Fig. 4 E

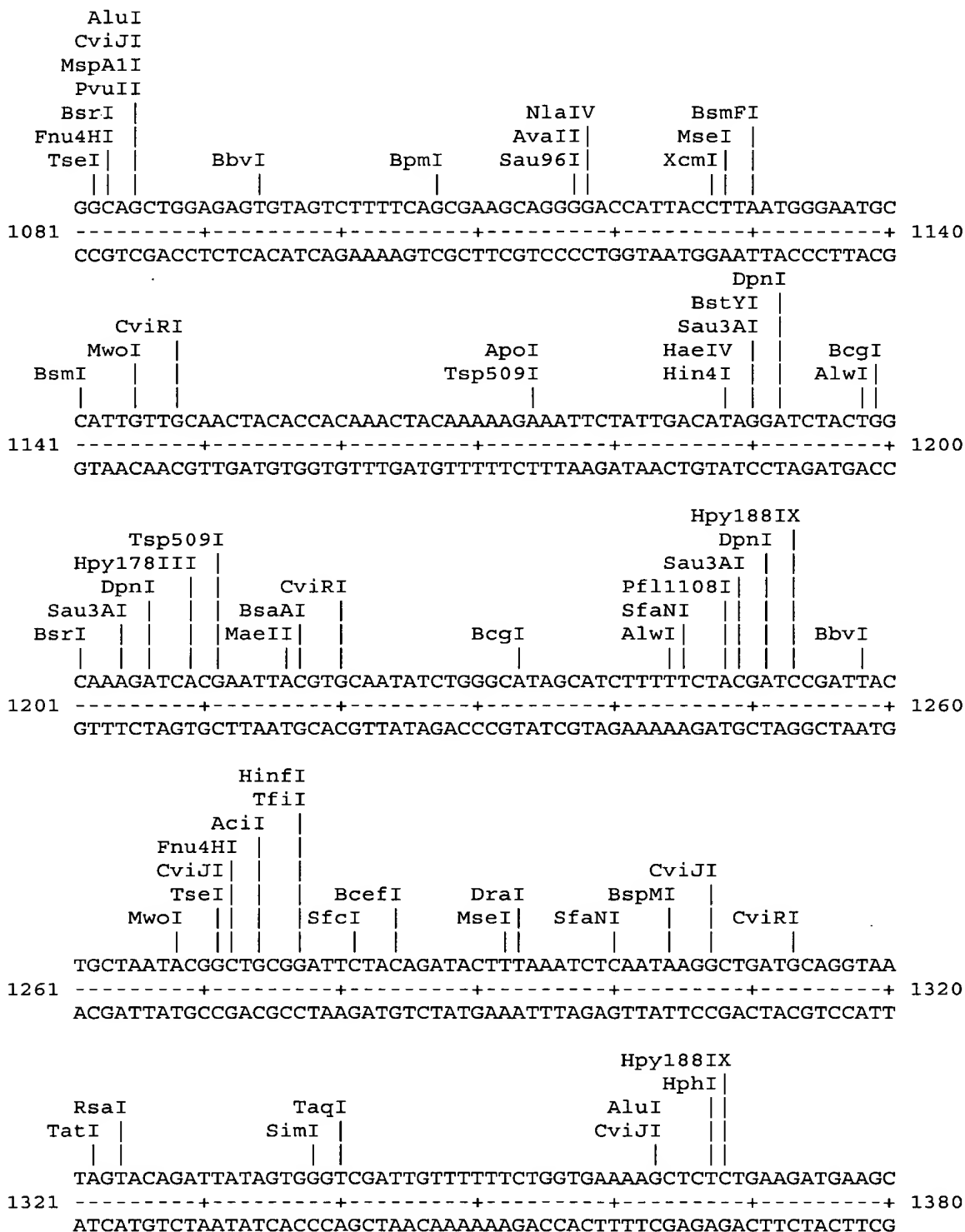
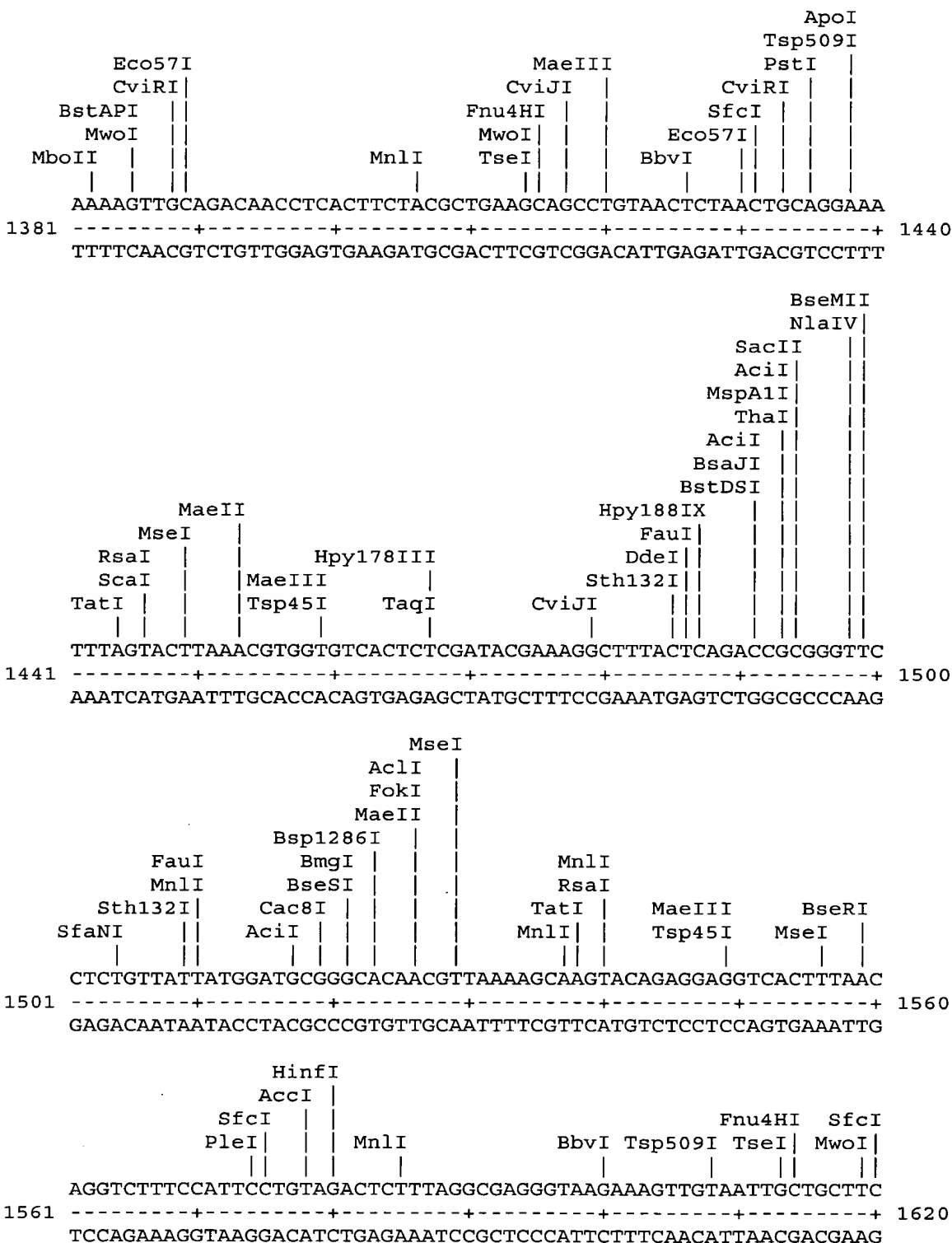




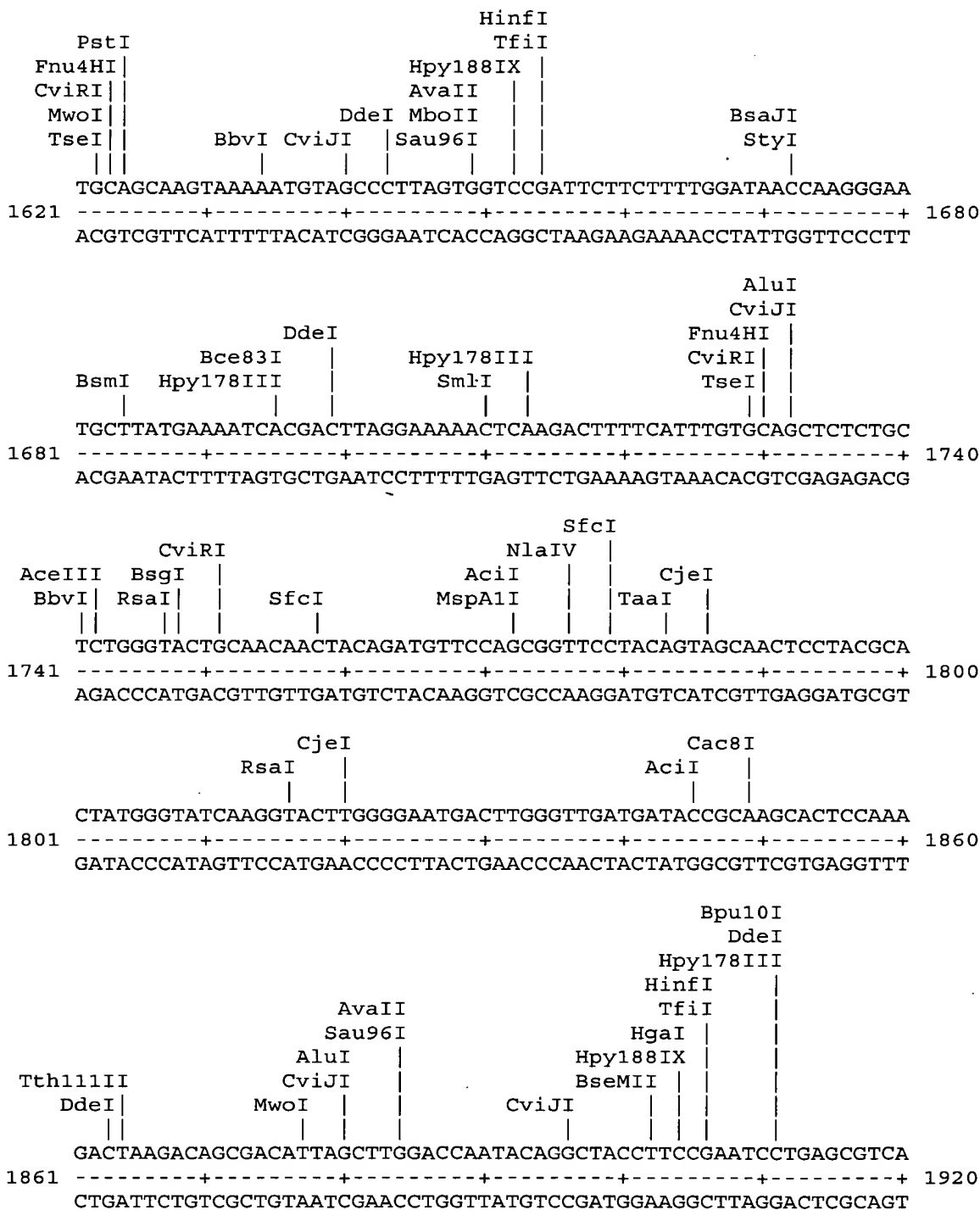
Fig. 4 F





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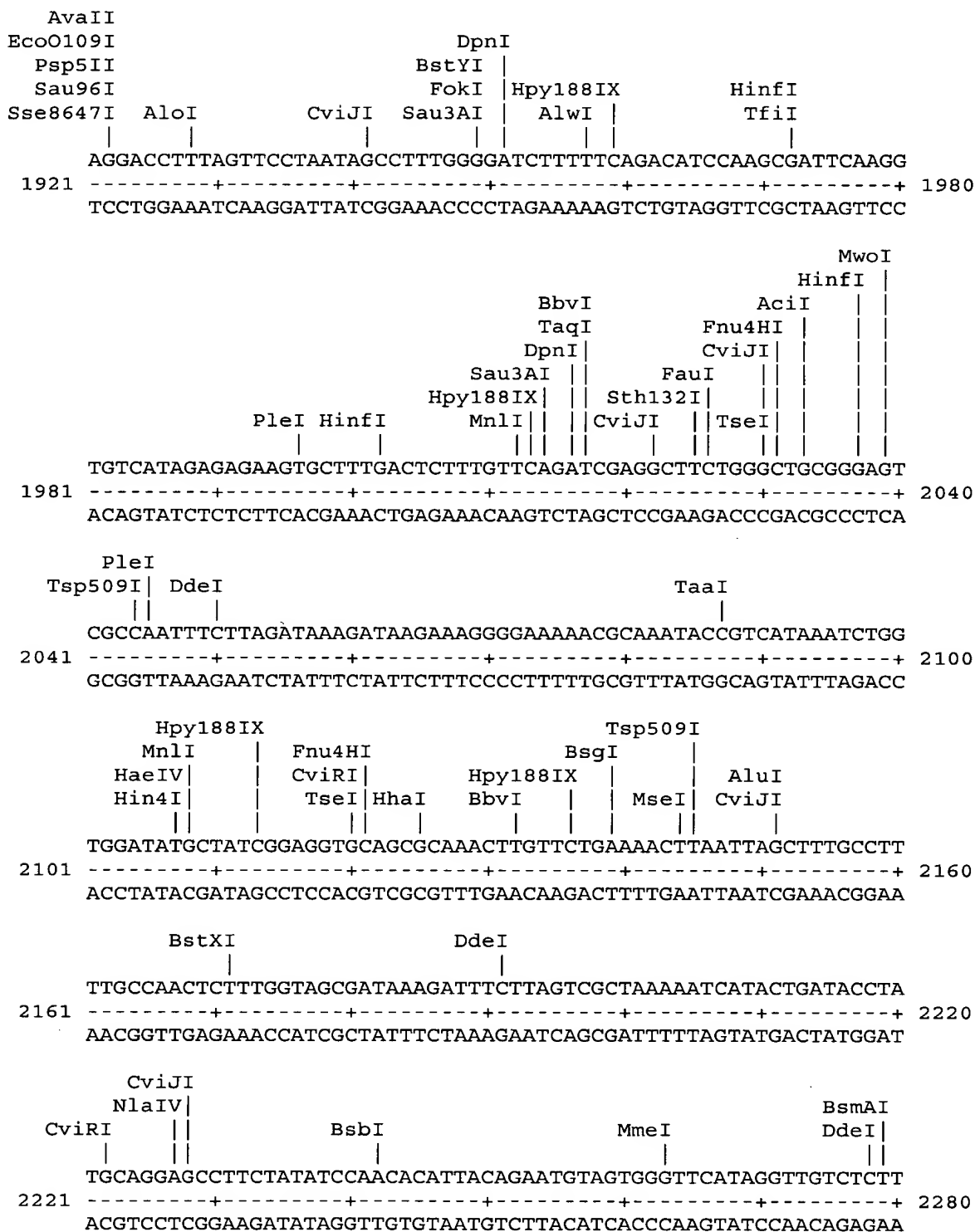
Fig. 4 G





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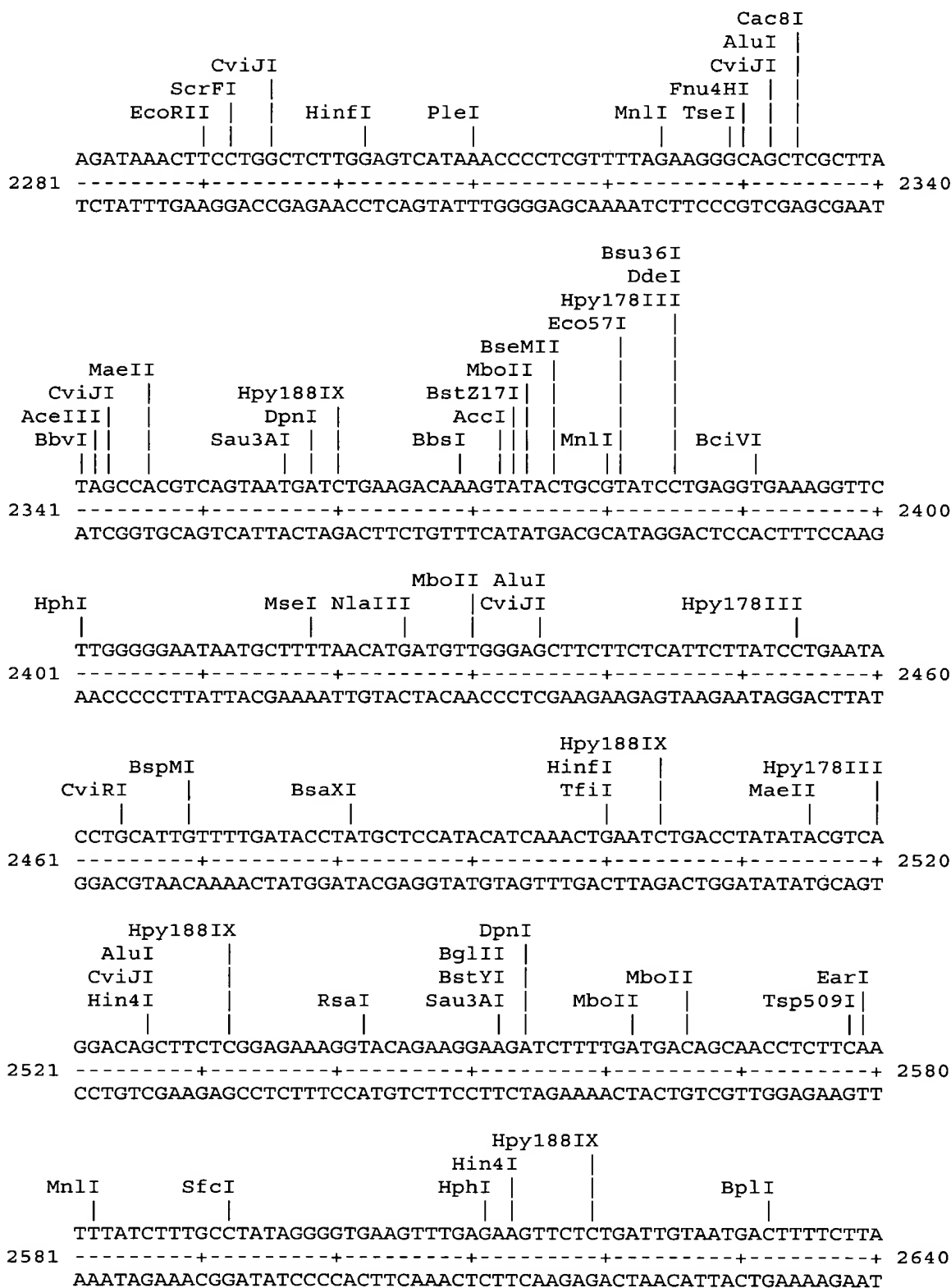
Fig. 4 H





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Fig. 4 I





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Fig. 4 J

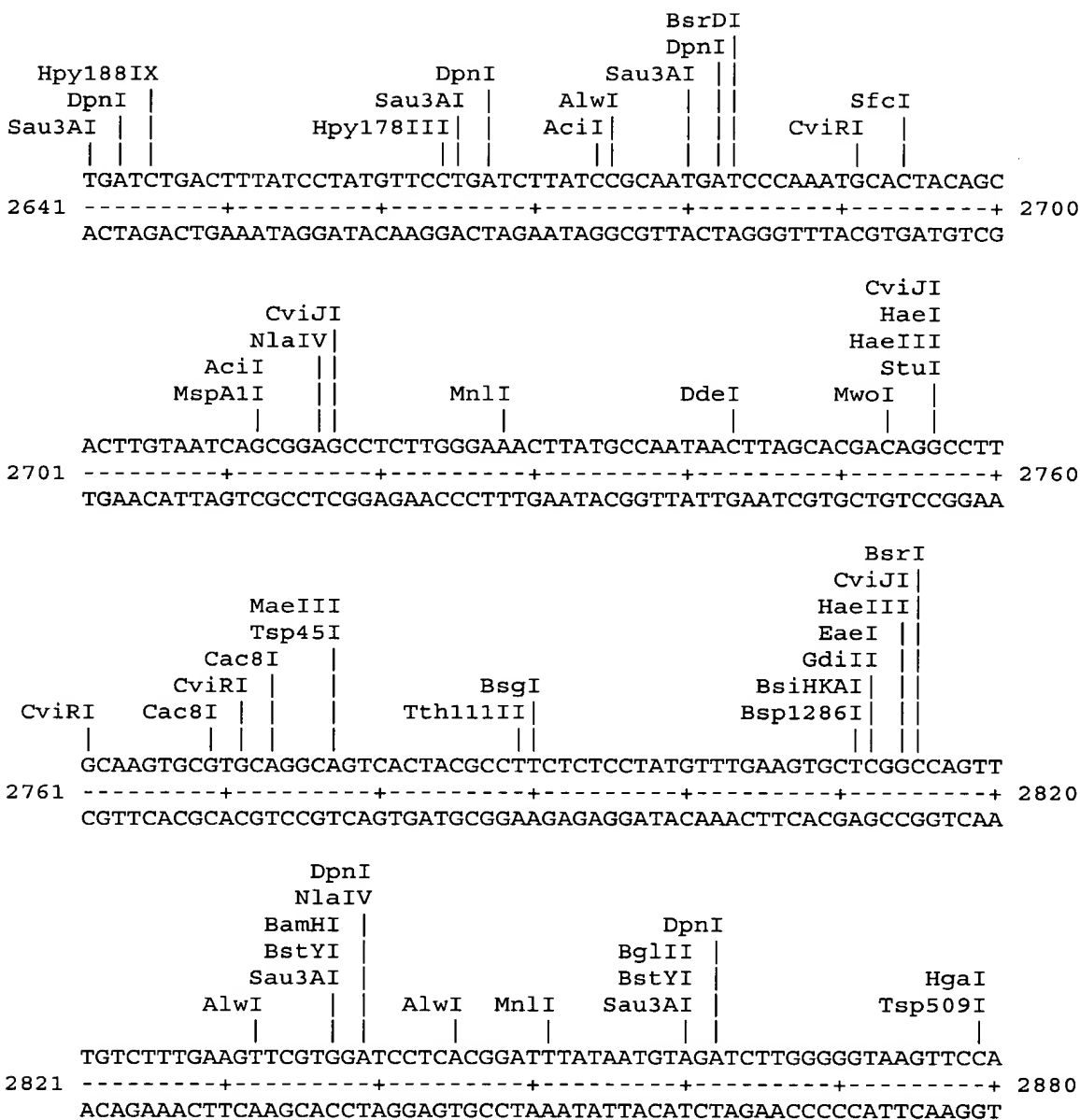




Fig. 4 K

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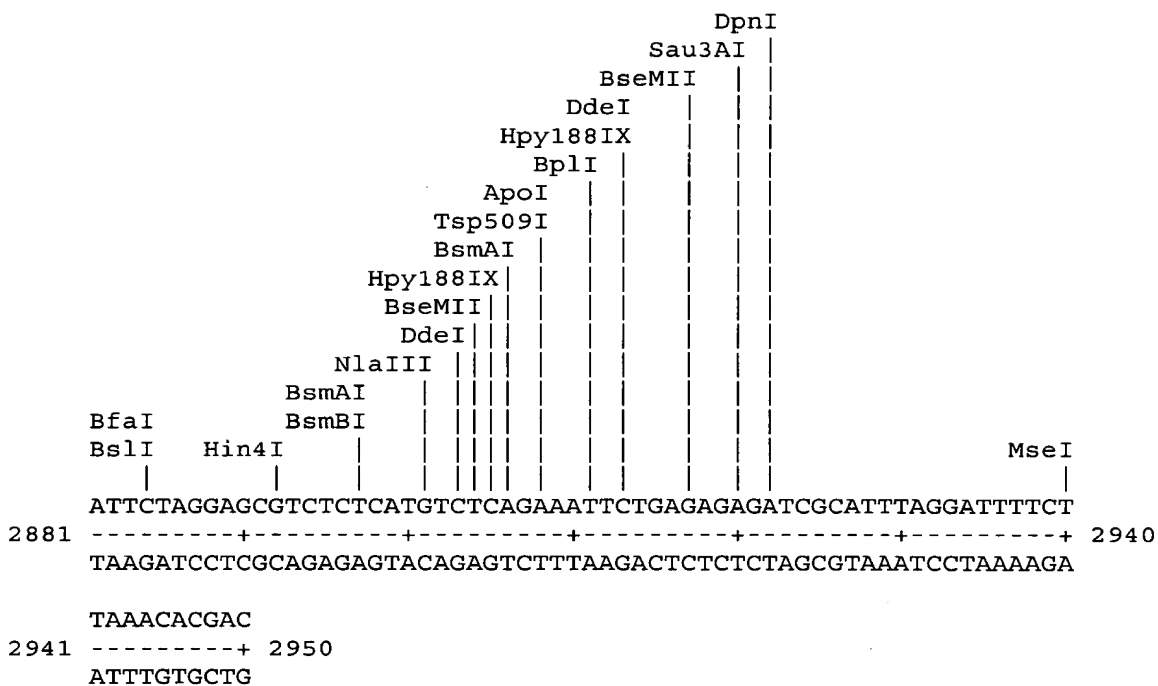




Figure 5 A: Nucleotide and deduced amino acid sequence of CPN100638

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Met Lys Ser Ser Leu
1 5
cat tgg ttt tta atc tcg tca tct tta gca ctt ccc ttg tca cta aat 163
His Trp Phe Leu Ile Ser Ser Ser Leu Ala Leu Pro Leu Ser Leu Asn
10 15 20
ttc tct gcg ttt gct gct gtt gtt gaa atc aat cta gga cct acc aat 211
Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn Leu Gly Pro Thr Asn
25 30 35
agc ttc tct gga cca gga acc tac act cct cca gcc caa aca aca aat 259
Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro Ala Gln Thr Thr Asn
40 45 50
gca gat gga act atc tat aat cta aca ggg gat gtc tca atc acc aat 307
Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp Val Ser Ile Thr Asn
55 60 65
gca gga tct ccg aca gct cta acc gct tcc tgc ttt aaa gaa act act 355
Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys Phe Lys Glu Thr Thr
70 75 80 85
ggg aat ctt tct ttc caa ggc cac ggc tac caa ttt ctc cta caa aat 403
Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln Phe Leu Leu Gln Asn
90 95 100
atc gat gcg gga gcg aac tgt acc ttt acc aat aca gct gca aat aag 451
Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn Thr Ala Ala Asn Lys
105 110 115
ctt ctc tcc ttt tca gga ttc tcc tat ttg tca cta ata caa acc acg 499
Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser Leu Ile Gln Thr Thr
120 125 130
aat gct acc aca gga aca gga gcc atc aag tcc aca gga gct tgt tct 547
Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser Thr Gly Ala Cys Ser
135 140 145
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Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln Asn Phe Ser Asn Asp
150 155 160 165
aat gga ggc gcc ctc caa ggc agc tct atc agt cta tcg cta aac ccc 643
Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser Leu Ser Leu Asn Pro
170 175 180
aac cta acg ttt gcc aaa aac aaa gca acg caa aaa ggg ggt gcc ctc 691
Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln Lys Gly Gly Ala Leu
185 190 195
```



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Fig. 5 B

tat	tcc	acg	gga	ggg	att	aca	att	aac	aat	acg	tta	aac	tca	gca	tca	739
Tyr	Ser	Thr	Gly	Gly	Ile	Thr	Ile	Asn	Asn	Thr	Leu	Asn	Ser	Ala	Ser	
		200					205					210				
ttt	tct	gaa	aat	acc	gcg	gcg	aac	aat	ggc	gga	gcc	att	tac	acg	gaa	787
Phe	Ser	Glu	Asn	Thr	Ala	Ala	Asn	Asn	Gly	Gly	Ala	Ile	Tyr	Thr	Glu	
		215				220					225					
gct	agc	agt	ttt	att	agc	agc	aac	aaa	gca	att	agc	ttt	ata	aac	aat	835
Ala	Ser	Ser	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Ile	Ser	Phe	Ile	Asn	Asn	
230					235					240					245	
agt	gtg	acc	gca	acc	tca	gct	aca	ggg	gga	gcc	att	tac	tgt	agt	agt	883
Ser	Val	Thr	Ala	Thr	Ser	Ala	Thr	Gly	Gly	Ala	Ile	Tyr	Cys	Ser	Ser	
				250					255						260	
aca	tca	gcc	ccc	aaa	cca	gtc	tta	act	cta	tca	gac	aac	ggg	gaa	ctg	931
Thr	Ser	Ala	Pro	Lys	Pro	Val	Leu	Thr	Leu	Ser	Asp	Asn	Gly	Glu	Leu	
			265					270					275			
aac	ttt	ata	gga	aat	aca	gca	att	act	agt	ggg	ggg	gcg	att	tat	act	979
Asn	Phe	Ile	Gly	Asn	Thr	Ala	Ile	Thr	Ser	Gly	Gly	Ala	Ile	Tyr	Thr	
		280					285					290				
gac	aat	cta	gtt	ctt	tct	tct	gga	gga	cct	acg	ctt	ttt	aaa	aac	aac	1027
Asp	Asn	Leu	Val	Leu	Ser	Ser	Gly	Gly	Pro	Thr	Leu	Phe	Lys	Asn	Asn	
	295					300					305					
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Ser	Gly	Tyr	Asp	Thr	Ala	Ala	Pro	Leu	Gly	Gly	Ala	Ile	Ala	Ile	Ala	
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gac	tct	gga	tct	ttg	agt	ctt	tcg	gct	ctt	ggg	gga	gac	atc	act	ttt	1123
Asp	Ser	Gly	Ser	Leu	Ser	Leu	Ser	Ala	Leu	Gly	Gly	Asp	Ile	Thr	Phe	
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gaa	gga	aac	aca	gta	gtc	aaa	gga	gct	tct	tcg	agt	cag	acc	act	acc	1171
Glu	Gly	Asn	Thr	Val	Val	Lys	Gly	Ala	Ser	Ser	Ser	Gln	Thr	Thr	Thr	
			345					350					355			
aga	aat	tct	att	aac	atc	gga	aac	acc	aat	gct	aag	att	gta	cag	ctg	1219
Arg	Asn	Ser	Ile	Asn	Ile	Gly	Asn	Thr	Asn	Ala	Lys	Ile	Val	Gln	Leu	
		360					365					370				
cga	gcc	tct	caa	ggc	aat	act	atc	tac	ttc	tat	gat	cct	ata	aca	act	1267
Arg	Ala	Ser	Gln	Gly	Asn	Thr	Ile	Tyr	Phe	Tyr	Asp	Pro	Ile	Thr	Thr	
		375				380					385					
agc	atc	act	gca	gct	ctc	tca	gat	gct	cta	aac	tta	aat	ggg	cct	gac	1315
Ser	Ile	Thr	Ala	Ala	Leu	Ser	Asp	Ala	Leu	Asn	Leu	Asn	Gly	Pro	Asp	
390					395				400						405	
ctt	gca	ggg	aat	cct	gca	tat	caa	gga	acc	atc	gta	ttt	tct	gga	gag	1363
Leu	Ala	Gly	Asn	Pro	Ala	Tyr	Gln	Gly	Thr	Ile	Val	Phe	Ser	Gly	Glu	
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Fig. 5 C

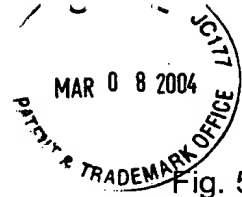
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tcg ctc tct ctt gta gat cct tct gga aat gtc tac gaa gat gtc tct	1699
Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val Tyr Glu Asp Val Ser	
520 525 530	
tgg aat aac cct caa gtc ttt tct tgt ctc act ctt act gct gac gac	1747
Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr Leu Thr Ala Asp Asp	
535 540 545	
ccc gcg aat att cac atc aca gac tta gct gct gat ccc cta gaa aaa	1795
Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala Asp Pro Leu Glu Lys	
550 555 560 565	
aat cct atc cat tgg gga tac caa ggg aat tgg gca tta tct tgg caa	1843
Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp Ala Leu Ser Trp Gln	
570 575 580	
gag gat act gcg act aaa tcc aaa gca gcg act ctt acc tgg aca aaa	1891
Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr Leu Thr Trp Thr Lys	
585 590 595	
aca gga tac aat ccg aat cct gag cgt cgt gga acc tta gtt gct aac	1939
Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly Thr Leu Val Ala Asn	
600 605 610	
acg cta tgg gga tcc ttt gtt gat gtg cgc tcc ata caa cag ctt gta	1987
Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile Gln Gln Leu Val	
615 620 625	
gcc act aaa gta cgc caa tct caa gaa act cgc ggc atc tgg tgt gaa	2035
Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg Gly Ile Trp Cys Glu	
630 635 640 645	



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Fig. 5 D

ggg atc tcg aac ttc ttc cat aaa gat agc acg aag ata aat aaa ggt	2083
Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr Lys Ile Asn Lys Gly	
650 655 660	
ttt cgc cac ata agt gca ggt tat gtt gta gga gcg act aca aca tta	2131
Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly Ala Thr Thr Thr Leu	
665 670 675	
gct tct gat aat ctt atc act gca gcc ttc tgc caa tta ttc ggg aaa	2179
Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys Gln Leu Phe Gly Lys	
680 685 690	
gat aga gat cac ttt ata aat aaa aat aga gct tct gcc tat gca gct	2227
Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala Ser Ala Tyr Ala Ala	
695 700 705	
tct ctc cat ctc cag cat cta gcg acc ttg tct tct cca agc ttg tta	2275
Ser Leu His Leu Gln His Leu Ala Thr Leu Ser Ser Pro Ser Leu Leu	
710 715 720 725	
cgc tac ctt cct gga tct gaa agt gag cag cct gtc ctc ttt gat gct	2323
Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro Val Leu Phe Asp Ala	
730 735 740	
cag atc agc tat atc tat agt aaa aat act atg aaa acc tat tac acc	2371
Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met Lys Thr Tyr Tyr Thr	
745 750 755	
caa gca cca aag gga gag agc tcg tgg tat aat gac ggt tgc gct ctg	2419
Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn Asp Gly Cys Ala Leu	
760 765 770	
gaa ctt gcg agc tcc cta cca cac act gct tta agc cat gag ggt ctc	2467
Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu Ser His Glu Gly Leu	
775 780 785	
ttc cac gcg tat ttt cct ttc atc aaa gta gaa gct tcg tac ata cac	2515
Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu Ala Ser Tyr Ile His	
790 795 800 805	
caa gat agc ttc aaa gaa cgt aat act acc ttg gta cga tct ttc gat	2563
Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu Val Arg Ser Phe Asp	
810 815 820	
agc ggt gat tta att aac gtc tct gtg cct att gga att acc ttc gag	2611
Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile Gly Ile Thr Phe Glu	
825 830 835	
aga ttc tcg aga aac gag cgt gcg tct tac gaa gct act gtc atc tac	2659
Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu Ala Thr Val Ile Tyr	
840 845 850	
gtt gcc gat gtc tat cgt aag aat cct gac tgc acg aca gct ctc cta	2707
Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys Thr Thr Ala Leu Leu	
855 860 865	



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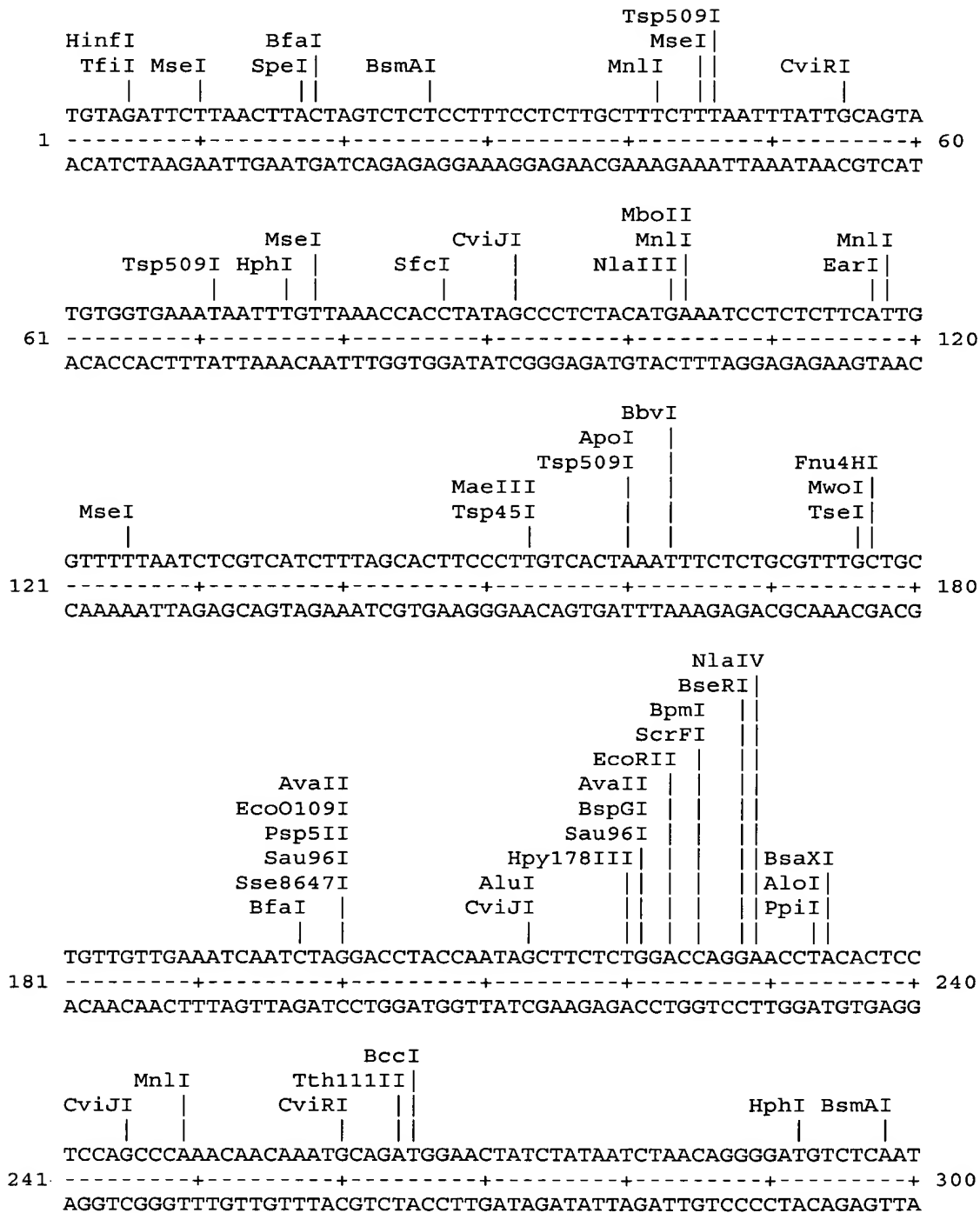
Fig. 5 E

atc aac aat acc tcg tgg aaa act aca gga acg aat ctc tca aga caa	2755
Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr Asn Leu Ser Arg Gln	
870 875 880 885	
gct ggt atc gga aga gca ggg atc ttt tat gcc ttc tct cca aat ctt	2803
Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala Phe Ser Pro Asn Leu	
890 895 900	
gag gtc aca agt aac cta tct atg gaa att cgt gga tct tca cgc agc	2851
Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg Gly Ser Ser Arg Ser	
905 910 915	
tac aat gca gat ctt gga ggt aag ttc cag ttc taaaagcggt cctgatccct	2904
Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe	
920 925	
tagaaattct aagagatcct gagtgtatct agggacttct caaaga	2950



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Figure 6 A: Restriction enzyme analysis of CPN100638





**REPLACEMENT SHEET**  
**Title: CHLAMYDIA ANTIGENS AND**  
**CORRESPONDING DNA FRAGMENTS AND**  
**USES THEREOF**  
**Inventor(s): Andrew D. MURDIN et al.**  
**Appl. No.: 09/857,128**



Fig. 6 D

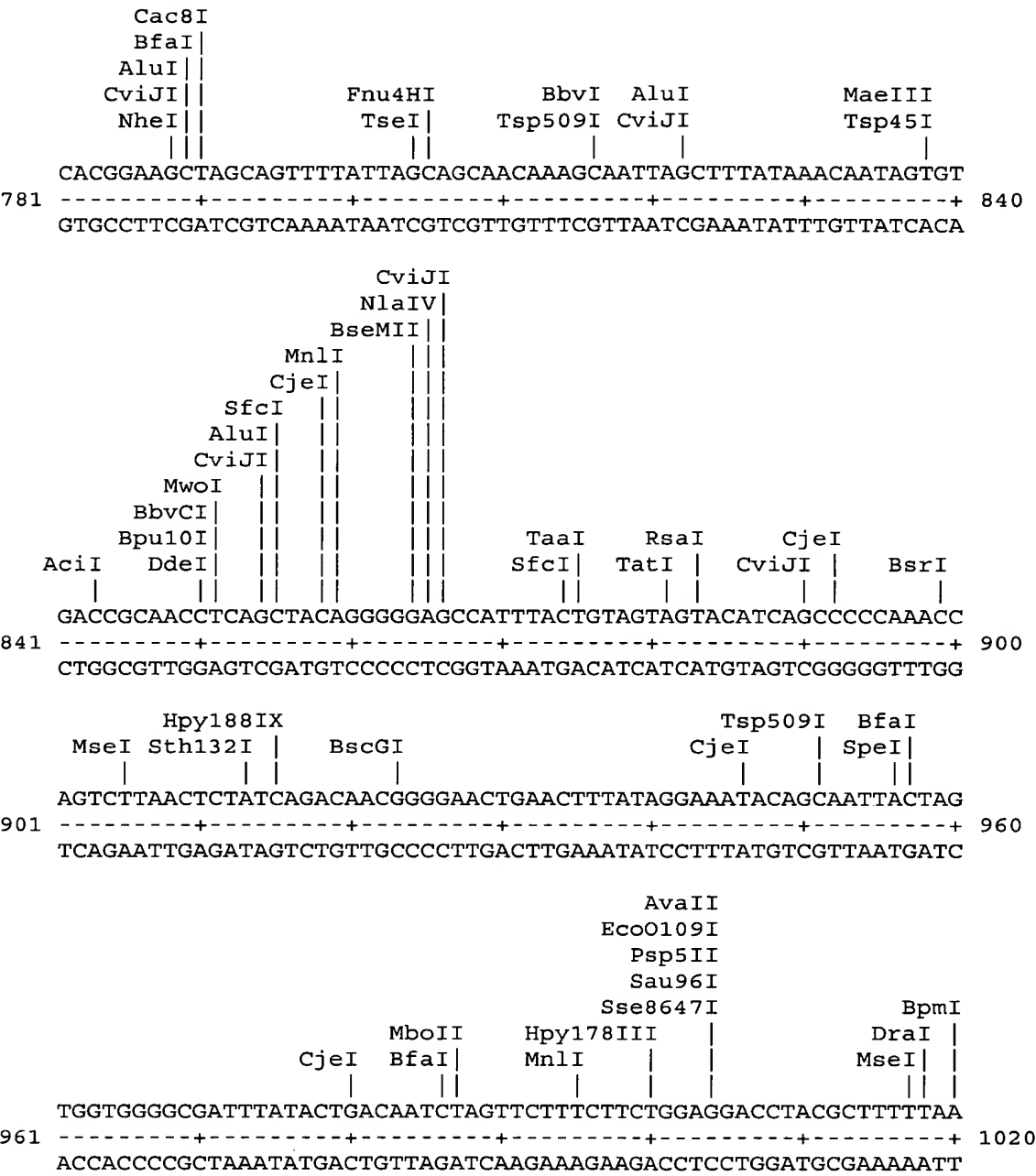
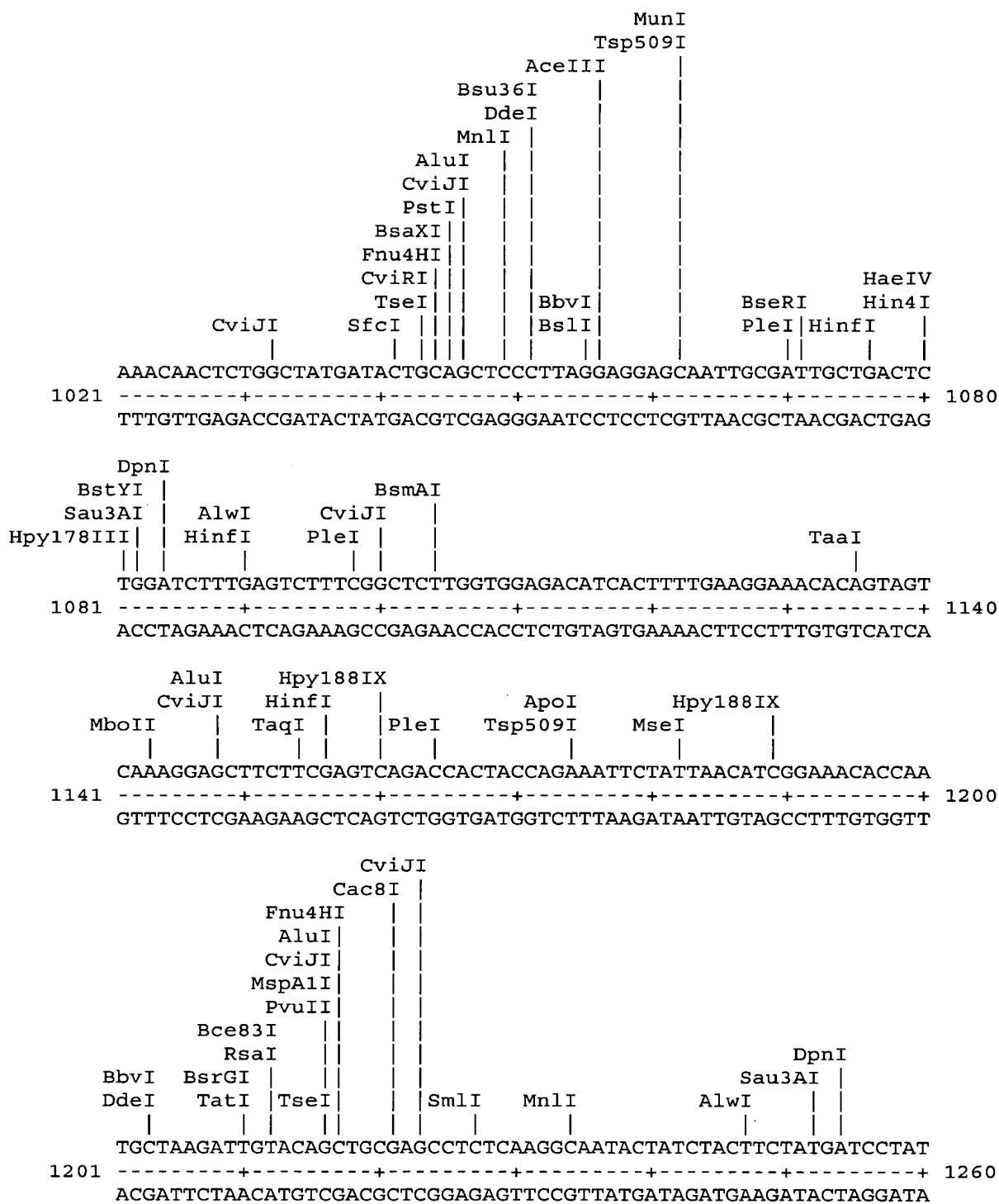


Fig. 6 E

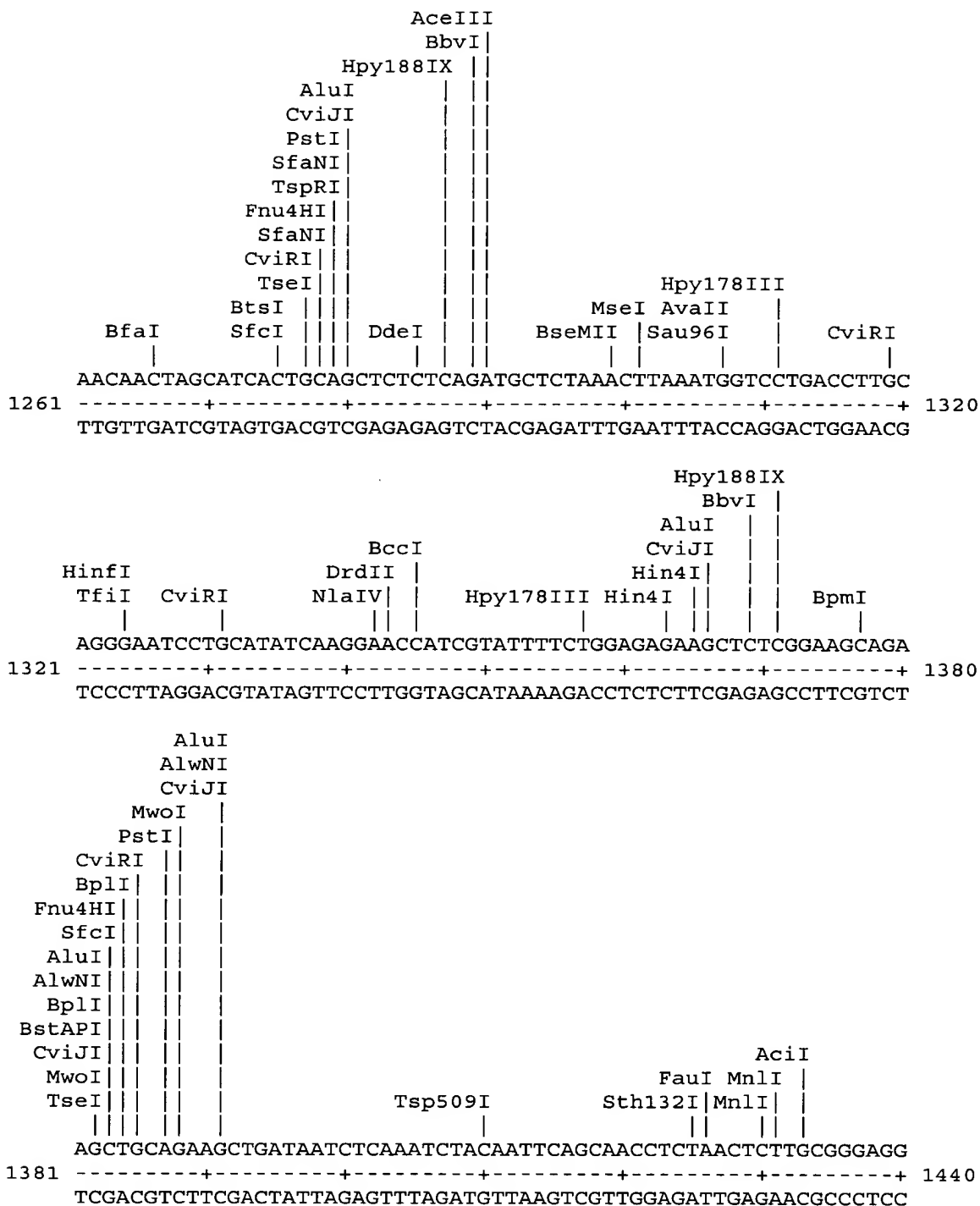


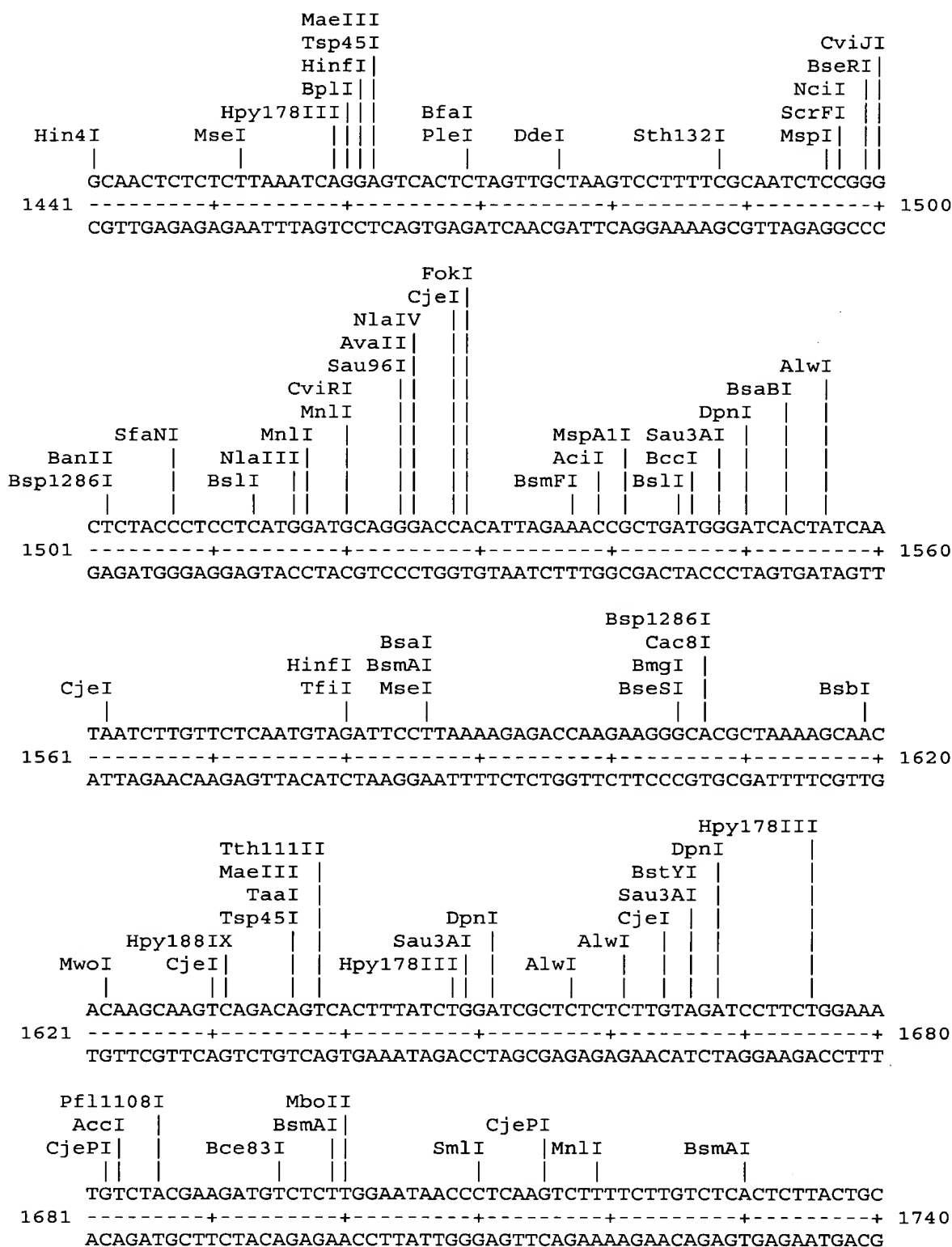
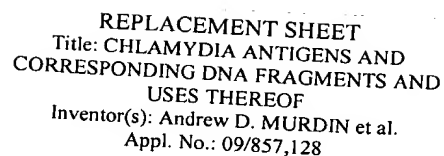




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Fig. 6 F

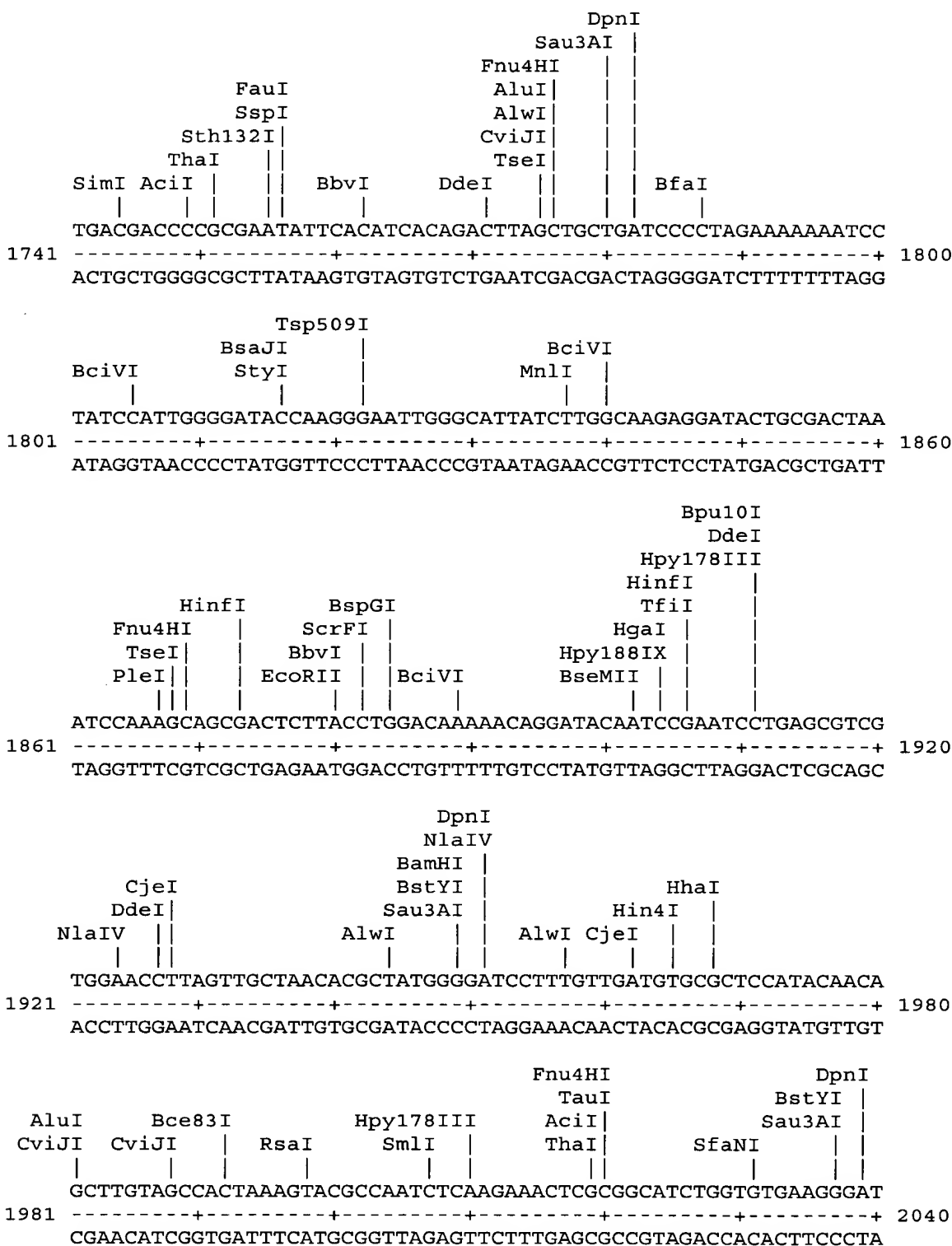






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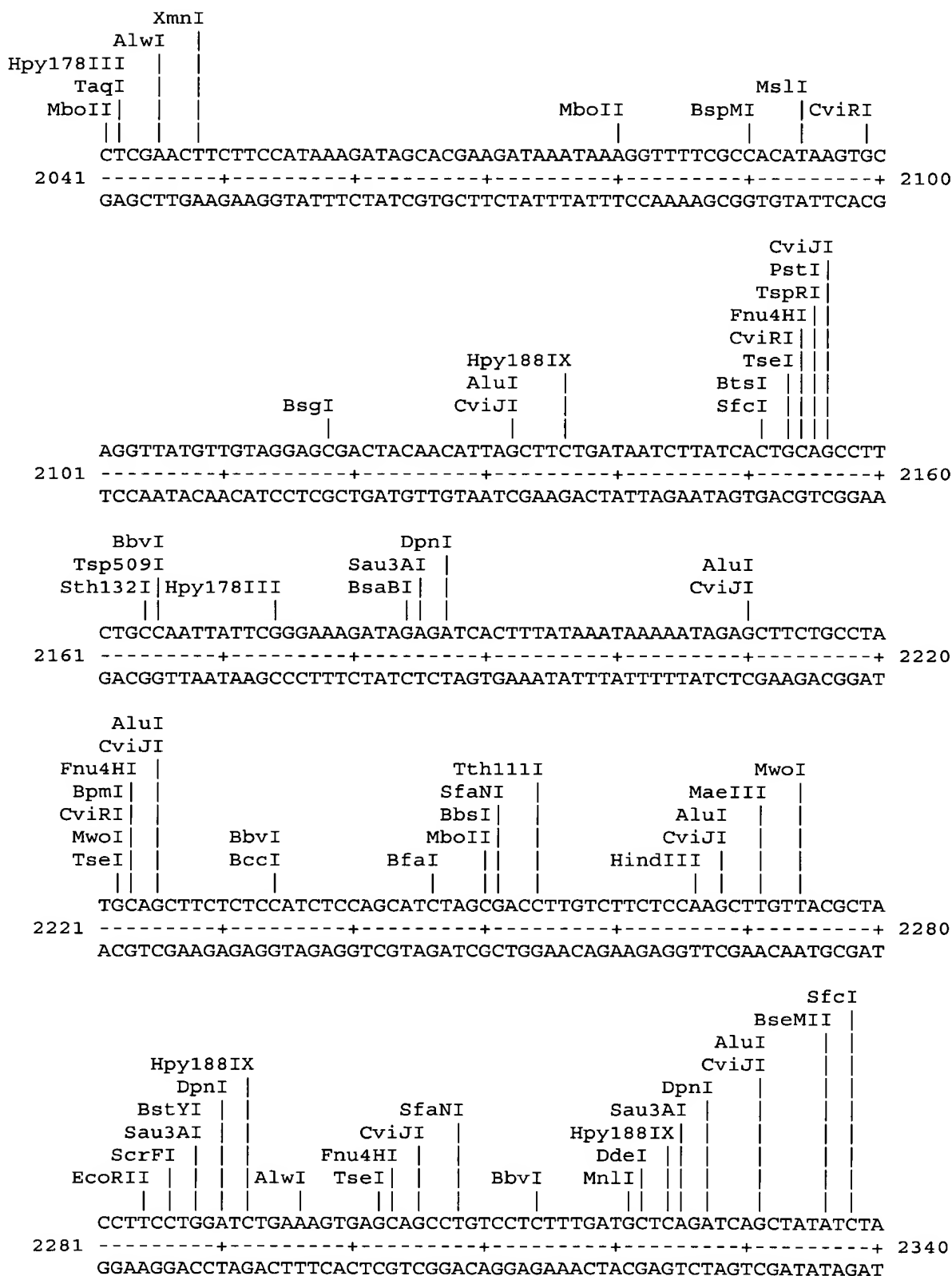
Fig. 6 H





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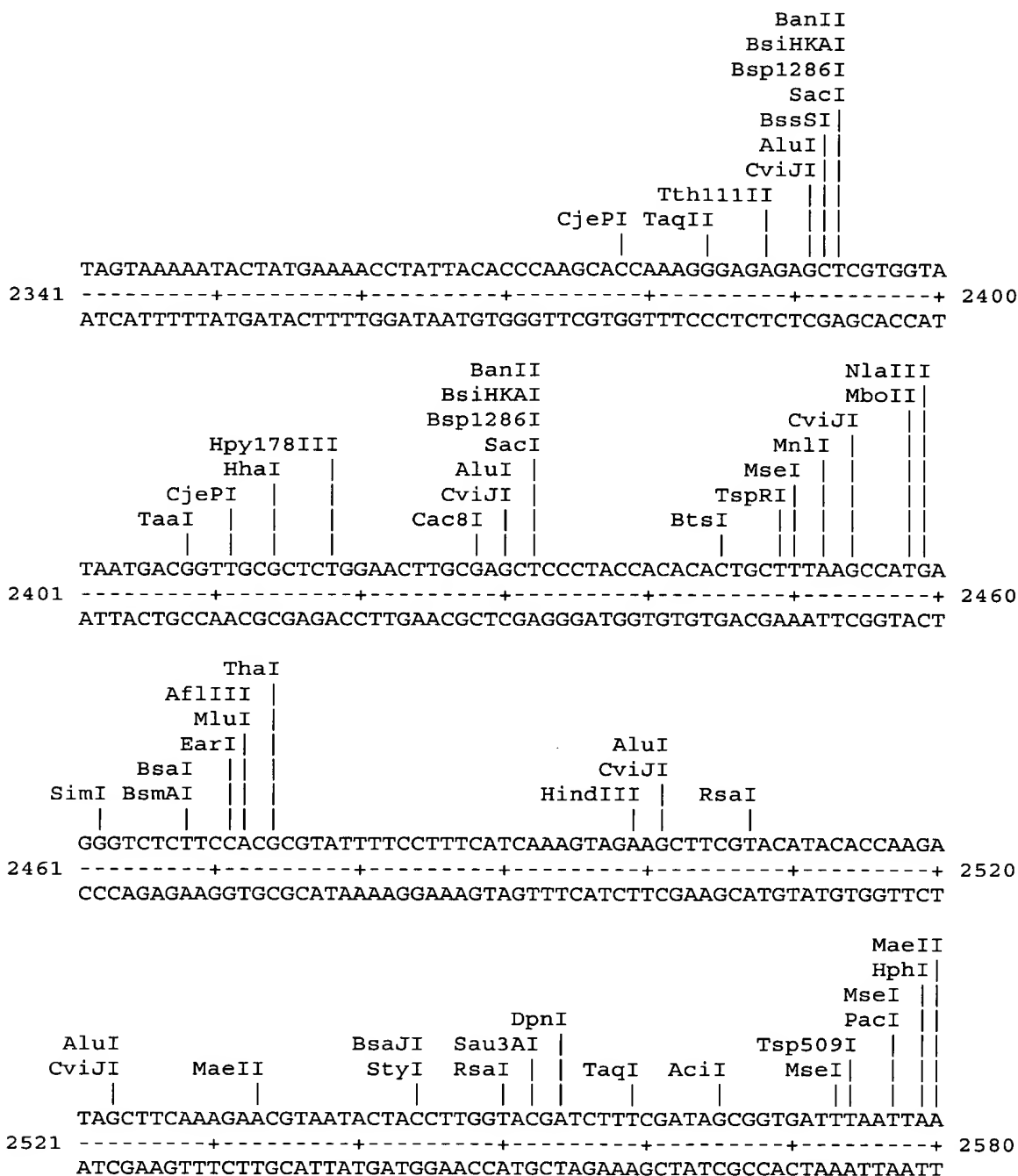
Fig. 6 I





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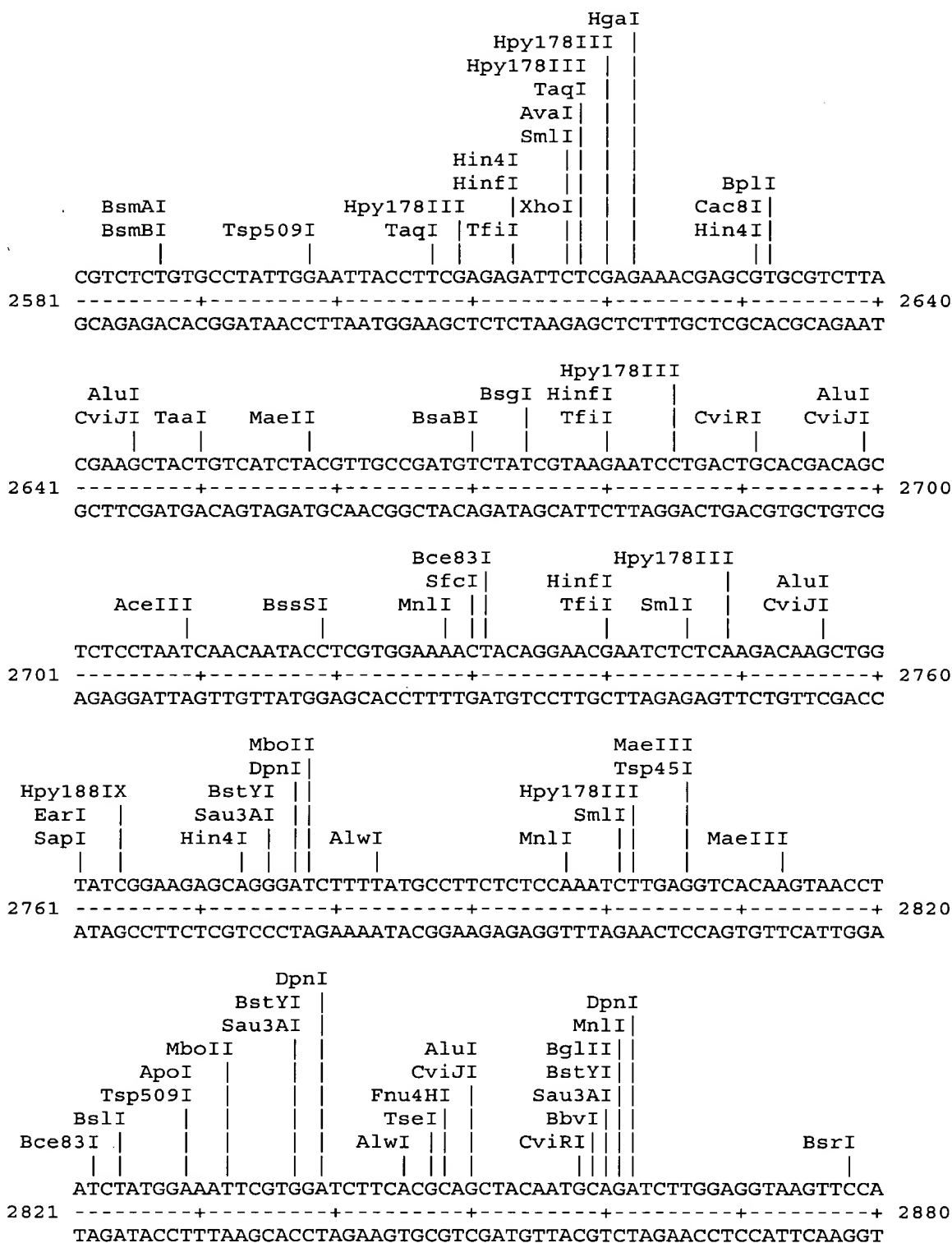
Fig. 6 J





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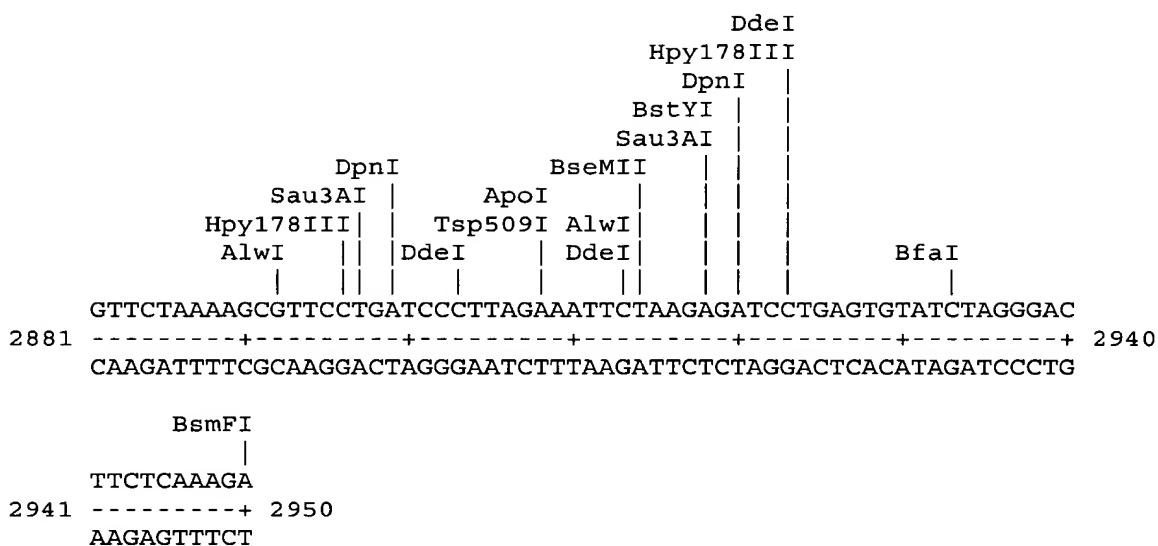
Fig. 6 K





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Fig. 6 L



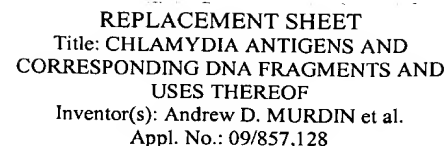
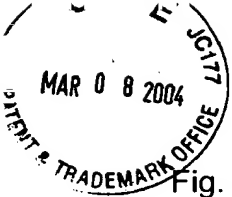


Figure 7 A: Nucleotide and amino acid sequence of CPN100639

gtacgaagtt	cttcacgaaa	ttataataca	aacctaggct	ctaagttttg	tttctagatt	60										
atcgaaaacg	tgттаattaa	ttgaacccaa	gcattctttct	atg	aaa	ata	ccc	ttg	115							
				Met	Lys	Ile	Pro	Leu								
				1				5								
cac	aaa	ctc	ctg	atc	tct	tcg	act	ctt	gtc	act	ccc	att	cta	ttg	agc	163
His	Lys	Leu	Leu	Ile	Ser	Ser	Thr	Leu	Val	Thr	Pro	Ile	Leu	Leu	Ser	
				10					15					20		
att	gca	act	tac	gga	gca	gat	gct	tct	tta	tcc	cct	aca	gat	agc	ttt	211
Ile	Ala	Thr	Tyr	Gly	Ala	Asp	Ala	Ser	Leu	Ser	Pro	Thr	Asp	Ser	Phe	
			25					30					35			
gat	gga	gcg	ggc	ggc	tct	aca	ttt	act	cca	aaa	tct	aca	gca	gat	gcc	259
Asp	Gly	Ala	Gly	Gly	Ser	Thr	Phe	Thr	Pro	Lys	Ser	Thr	Ala	Asp	Ala	
		40					45					50				
aat	gga	acg	aac	tat	gtc	tta	tca	gga	aat	gtc	tat	ata	aac	gat	gct	307
Asn	Gly	Thr	Asn	Tyr	Val	Leu	Ser	Gly	Asn	Val	Tyr	Ile	Asn	Asp	Ala	
	55					60					65					
ggg	aaa	ggc	aca	gca	tta	aca	ggc	tgc	tgc	ttt	aca	gaa	act	acg	ggc	355
Gly	Lys	Gly	Thr	Ala	Leu	Thr	Gly	Cys	Cys	Phe	Thr	Glu	Thr	Thr	Gly	
70					75					80					85	
gat	ctg	aca	ttt	act	gga	aag	gga	tac	tca	ttt	tca	ttc	aac	acg	gta	403
Asp	Leu	Thr	Phe	Thr	Gly	Lys	Gly	Tyr	Ser	Phe	Ser	Phe	Asn	Thr	Val	
				90					95					100		
gat	gcg	ggt	tcg	aat	gca	gga	gct	gcg	gca	agc	aca	act	gct	gat	aaa	451
Asp	Ala	Gly	Ser	Asn	Ala	Gly	Ala	Ala	Ala	Ser	Thr	Thr	Ala	Asp	Lys	
			105					110					115			
gcc	cta	atc	ttc	aca	gga	ttt	tct	aac	ctt	tcc	ttc	att	gca	gct	cct	499
Ala	Leu	Ile	Phe	Thr	Gly	Phe	Ser	Asn	Leu	Ser	Phe	Ile	Ala	Ala	Pro	
		120					125					130				
gga	act	aca	gtt	gct	tca	gga	aaa	agt	act	tta	agt	tct	gca	gga	gcc	547
Gly	Thr	Thr	Val	Ala	Ser	Gly	Lys	Ser	Thr	Leu	Ser	Ser	Ala	Gly	Ala	
	135					140					145					
tta	aat	ctt	acc	gat	aat	gga	acg	att	ctc	ttt	agc	caa	aac	gtc	tcc	595
Leu	Asn	Leu	Thr	Asp	Asn	Gly	Thr	Ile	Leu	Phe	Ser	Gln	Asn	Val	Ser	
150					155					160					165	
aat	gaa	gct	aat	aac	aat	ggc	gga	gcg	atc	acc	aca	aaa	act	ctt	tct	643
Asn	Glu	Ala	Asn	Asn	Asn	Gly	Gly	Ala	Ile	Thr	Thr	Lys	Thr	Leu	Ser	
				170					175					180		
att	tct	ggg	aat	acc	tct	tct	ata	acc	ttc	act	agt	aat	agc	gca	aaa	691
Ile	Ser	Gly	Asn	Thr	Ser	Ser	Ile	Thr	Phe	Thr	Ser	Asn	Ser	Ala	Lys	
			185					190					195			





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Fig. 7 B

aaa tta ggt gga gcg atc tat agc tct gcg gct gca agt att tca gga	739
Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala Ala Ser Ile Ser Gly	
200 205 210	
aac acc ggc cag tta gtc ttt atg aat aat aaa gga gaa act ggg ggt	787
Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys Gly Glu Thr Gly Gly	
215 220 225	
ggg gct ctg ggc ttt gaa gcc agc tcc tcg att act caa aat agc tcc	835
Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile Thr Gln Asn Ser Ser	
230 235 240 245	
ctt ttc ttc tct gga aac act gca aca gat gct gca ggc aag ggc ggg	883
Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala Ala Gly Lys Gly Gly	
250 255 260	
gcc att tat tgt gaa aaa aca gga gag act cct act ctt act atc tct	931
Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro Thr Leu Thr Ile Ser	
265 270 275	
gga aat aaa agt ctg acc ttc gcc gag aac tct tca gta act caa ggc	979
Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser Ser Val Thr Gln Gly	
280 285 290	
gga gca atc tgt gcc cat ggt cta gat ctt tcc gct gct ggc cct acc	1027
Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser Ala Ala Gly Pro Thr	
295 300 305	
cta ttt tca aat aat aga tgc ggg aac aca gct gca ggc aag ggc ggc	1075
Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala Ala Gly Lys Gly Gly	
310 315 320 325	
gct att gca att gcc gac tct gga tct tta agt ctc tct gca aat caa	1123
Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Asn Gln	
330 335 340	
gga gac atc acg ttc ctt ggc aac act cta acc tca acc tcc gcg cca	1171
Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr Ser Thr Ser Ala Pro	
345 350 355	
aca tcg aca cgg aat gct atc tac ctg gga tcg tca gca aaa att acg	1219
Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser Ser Ala Lys Ile Thr	
360 365 370	
aac tta agg gca gcc caa ggc caa tct atc tat ttc tat gat ccg att	1267
Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr Phe Tyr Asp Pro Ile	
375 380 385	
gca tct aac acc aca gga gct tca gac gtt ctg acc atc aac caa ccg	1315
Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu Thr Ile Asn Gln Pro	
390 395 400 405	
gat agc aac tcg cct tta gat tat tca gga acg att gta ttt tct ggg	1363
Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr Ile Val Phe Ser Gly	
410 415 420	



Fig. 7 C

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gaa aag ctc tct gca gat gaa gcg aaa gct gct gat aac ttc aca tct	1411
Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala Asp Asn Phe Thr Ser	
425 430 435	
ata tta aag caa cca ttg gct cta gcc tct gga acc tta gca ctc aaa	1459
Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly Thr Leu Ala Leu Lys	
440 445 450	
gga aat gtc gag tta gat gtc aat ggt ttc aca cag act gaa ggc tct	1507
Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr Gln Thr Glu Gly Ser	
455 460 465	
aca ctc ctc atg caa cca gga aca aag ctc aaa gca gat act gaa gct	1555
Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys Ala Asp Thr Glu Ala	
470 475 480 485	
atc agt ctt acc aaa ctt gtc gtt gat ctt tct gcc tta gag gga aat	1603
Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser Ala Leu Glu Gly Asn	
490 495 500	
aag agt gtg tcc att gaa aca gca gga gcc aac aaa act ata act cta	1651
Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn Lys Thr Ile Thr Leu	
505 510 515	
acc tct cct ctt gtt ttc caa gat agt agc ggc aat ttt tat gaa agc	1699
Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly Asn Phe Tyr Glu Ser	
520 525 530	
cat acg ata aac caa gcc ttc acg cag cct ttg gtg gta ttc act gct	1747
His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu Val Val Phe Thr Ala	
535 540 545	
gct act gct gct agc gat att tat atc gat gcg ctt ctc act tct cca	1795
Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala Leu Leu Thr Ser Pro	
550 555 560 565	
gta caa act cca gaa cct cat tac ggg tat cag gga cat tgg gaa gcc	1843
Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln Gly His Trp Glu Ala	
570 575 580	
act tgg gca gac aca tca act gca aaa tca gga act atg act tgg gta	1891
Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly Thr Met Thr Trp Val	
585 590 595	
act acg ggc tac aac cct aat cct gag cgt aga gct tcc gta gtt ccc	1939
Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Ala Ser Val Val Pro	
600 605 610	
gat tca tta tgg gca tcc ttt act gac att cgc act cta cag cag atc	1987
Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg Thr Leu Gln Gln Ile	
615 620 625	
atg aca tct caa gcg aat agt atc tat cag caa cga gga ctc tgg gca	2035
Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln Arg Gly Leu Trp Ala	
630 635 640 645	



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Fig. 7 D

tca gga act gcg aat ttc ttc cat aag gat aaa tca gga act aac caa	2083
Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys Ser Gly Thr Asn Gln	
650 655 660	
gca ttc cga cat aaa agc tac ggc tat att gtt gga gga agt gct gaa	2131
Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val Gly Gly Ser Ala Glu	
665 670 675	
gat ttt tct gaa aat atc ttc agt gta gct ttc tgc cag ctc ttc ggt	2179
Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe Cys Gln Leu Phe Gly	
680 685 690	
aaa gat aaa gac ctg ttt ata gtt gaa aat acc tct cat aac tat tta	2227
Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr Ser His Asn Tyr Leu	
695 700 705	
gcg tcg cta tac ctg caa cat cga gca ttc cta gga gga ctt ccc atg	2275
Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu Gly Gly Leu Pro Met	
710 715 720 725	
ccc tca ttt gga agt atc acc gac atg ctg aaa gat att cct ctc att	2323
Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys Asp Ile Pro Leu Ile	
730 735 740	
ttg aat gcc cag cta agc tac agc tac act aaa aat gat atg gat act	2371
Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys Asn Asp Met Asp Thr	
745 750 755	
cgc tat act tcc tat cct gaa gct caa ggc tct tgg acc aat aac tct	2419
Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser Trp Thr Asn Asn Ser	
760 765 770	
ggg gct cta gag ctc gga gga tct ctg gct cta tat ctc cct aaa gaa	2467
Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu Tyr Leu Pro Lys Glu	
775 780 785	
gca ccg ttc ttc cag gga tat ttc ccc ttc tta aag ttc cag gca gtc	2515
Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu Lys Phe Gln Ala Val	
790 795 800 805	
tac agc cgc caa caa aac ttt aaa gag agt ggc gct gaa gcc cgt gct	2563
Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly Ala Glu Ala Arg Ala	
810 815 820	
ttt gat gat gga gac cta gtg aac tgc tct atc cct gtc ggc att cgg	2611
Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile Pro Val Gly Ile Arg	
825 830 835	
tta gaa aaa atc tcc gaa gat gaa aaa aat aat ttc gag att tct cta	2659
Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn Phe Glu Ile Ser Leu	
840 845 850	
gcc tac att ggt gat gtg tat cgt aaa aat ccc cgt tcg cgt act tct	2707
Ala Tyr Ile Gly Asp Val Tyr Arg Lys Asn Pro Arg Ser Arg Thr Ser	
855 860 865	



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Fig. 7 E

cta atg gtc agt gga gcc tct tgg act tcg cta tgt aaa aac ctc gca	2755
Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu Cys Lys Asn Leu Ala	
870 875 880 885	
cga caa gcc ttc tta gca agt gct gga agc cat ctg act ctc tcc cct	2803
Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His Leu Thr Leu Ser Pro	
890 895 900	
cat gta gaa ctc tct ggg gaa gct gct tat gag ctt cgt ggc tca gca	2851
His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu Leu Arg Gly Ser Ala	
905 910 915	
cac atc tac aat gta gat tgt ggg cta aga tac tca ttc tagttcctac	2900
His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr Ser Phe	
920 925 930	
tttcctccct aaacttttag ggaggaattc ttataaaaac cctgtagatt cttaacttac	2960
tagtctctcc tttcctcttg ctttctttaa tttattgcag	3000



Figure 8 A: Restriction enzyme analysis of CPN100639

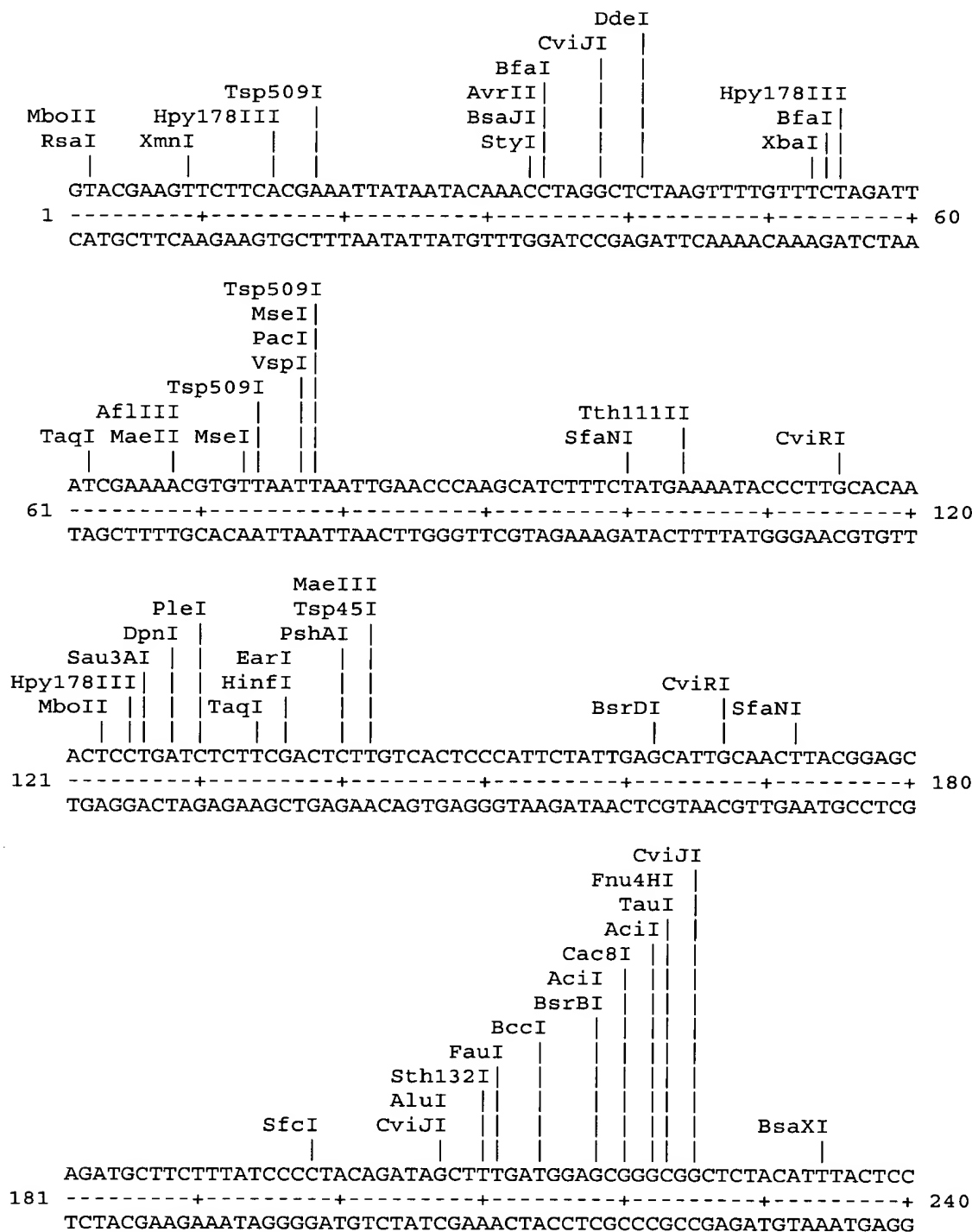


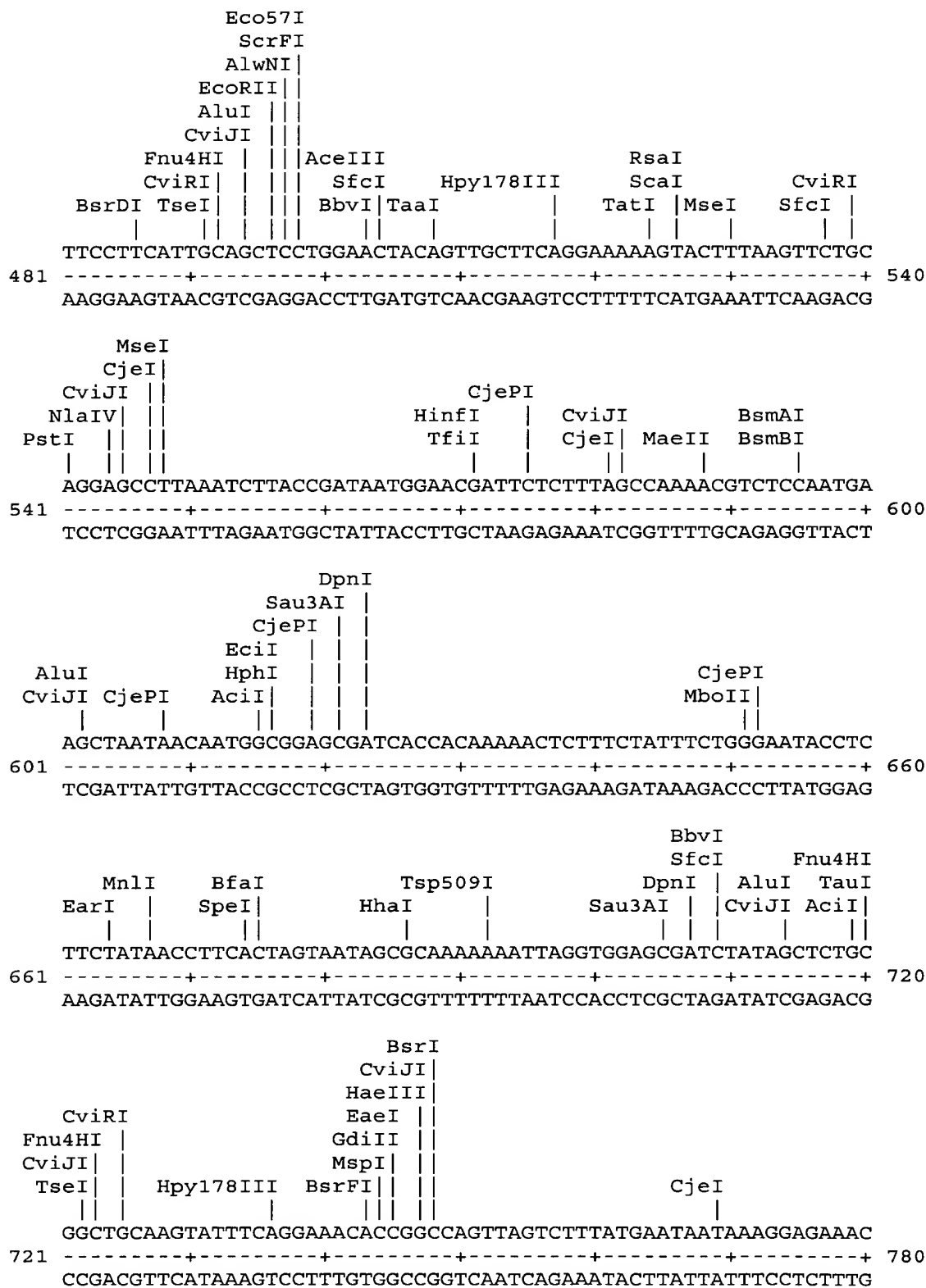
Fig. 8 B

SfcI  
 SfaNI  
 Hpy178III  
 SfaNI  
 241  
 AAAATCTACAGCAGATGCCAATGGAACGAACTATGTCTTATCAGGAAATGTCTATATAAA  
 -----+-----+-----+-----+-----+-----+ 300  
 TTTTAGATGTCGTCTACGGTTACCTTGCTTGATACAGAATAGTCCTTTACAGATATATTT  
 Hpy188IX  
 DpnI  
 Fnu4HI  
 TseI  
 MseI  
 Fnu4HI  
 TseI  
 BbvI  
 BbvI  
 Sth132I  
 Sau3AI  
 BscGI  
 Bsp24I  
 CjeI  
 CjePI  
 301  
 CGATGCTGGGAAAGGCACAGCATTAAACAGGCTGCTGCTTTACAGAACTACGGGTGATCT  
 -----+-----+-----+-----+-----+-----+ 360  
 GCTACGACCCTTTCCGTGTCGTAATTGTCCGACGACGAAATGTCTTTGATGCCACTAGA  
 FauI  
 TaaI  
 NspV  
 TaqI  
 BbvI  
 CjeI  
 CjePI  
 Bsp24I  
 SfaNI  
 Sth132I  
 BsbI  
 AceIII  
 Acil  
 CviRI  
 361  
 GACATTTACTGGAAAGGGATACTCATTTTCATTCAACACGGTAGATGCGGGTTCGAATGC  
 -----+-----+-----+-----+-----+-----+ 420  
 CTGTAAATGACCTTTCCCTATGAGTAAAGTAAGTTGTGCCATCTACGCCCCAGCTTACG  
 Cac8I  
 Fnu4HI  
 TauI  
 Acil  
 Fnu4HI  
 AluI  
 AlwNI  
 BstAPI  
 CviJI  
 MwoI  
 TseI  
 BsmI  
 CviJI  
 MboII  
 MwoI  
 Tth111III  
 421  
 AGGAGCTGCGGCAAGCACAACTGCTGATAAAGCCCTAATCTTCACAGGATTTTCTAACCT  
 -----+-----+-----+-----+-----+-----+ 480  
 TCCTCGACGCCGTTTCGTGTTGACGACTATTTTCGGGATTAGAAGTGTCTTAAAGATTGGA



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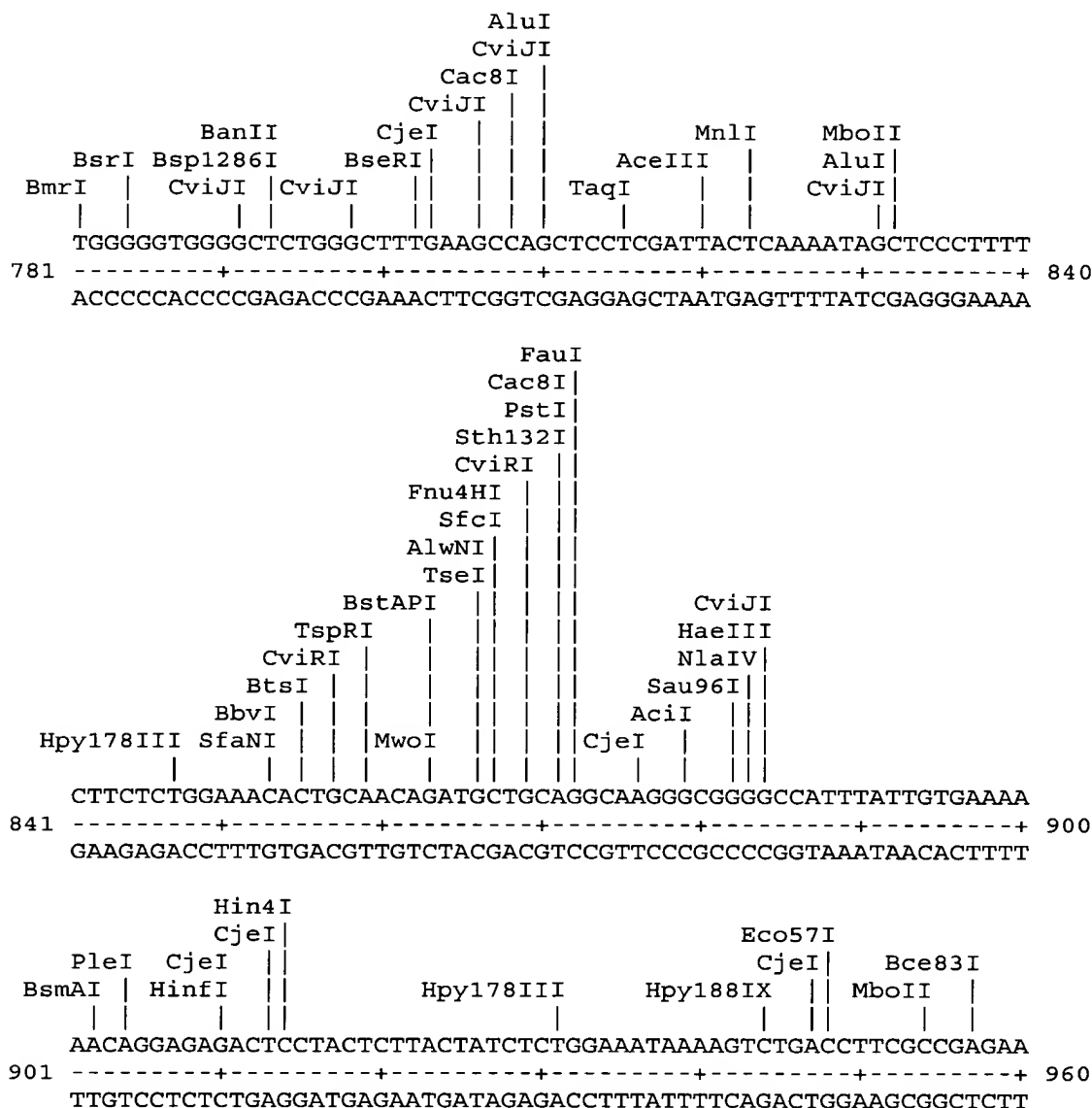
Fig. 8 C





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Fig. 8 D





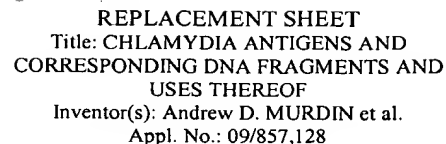
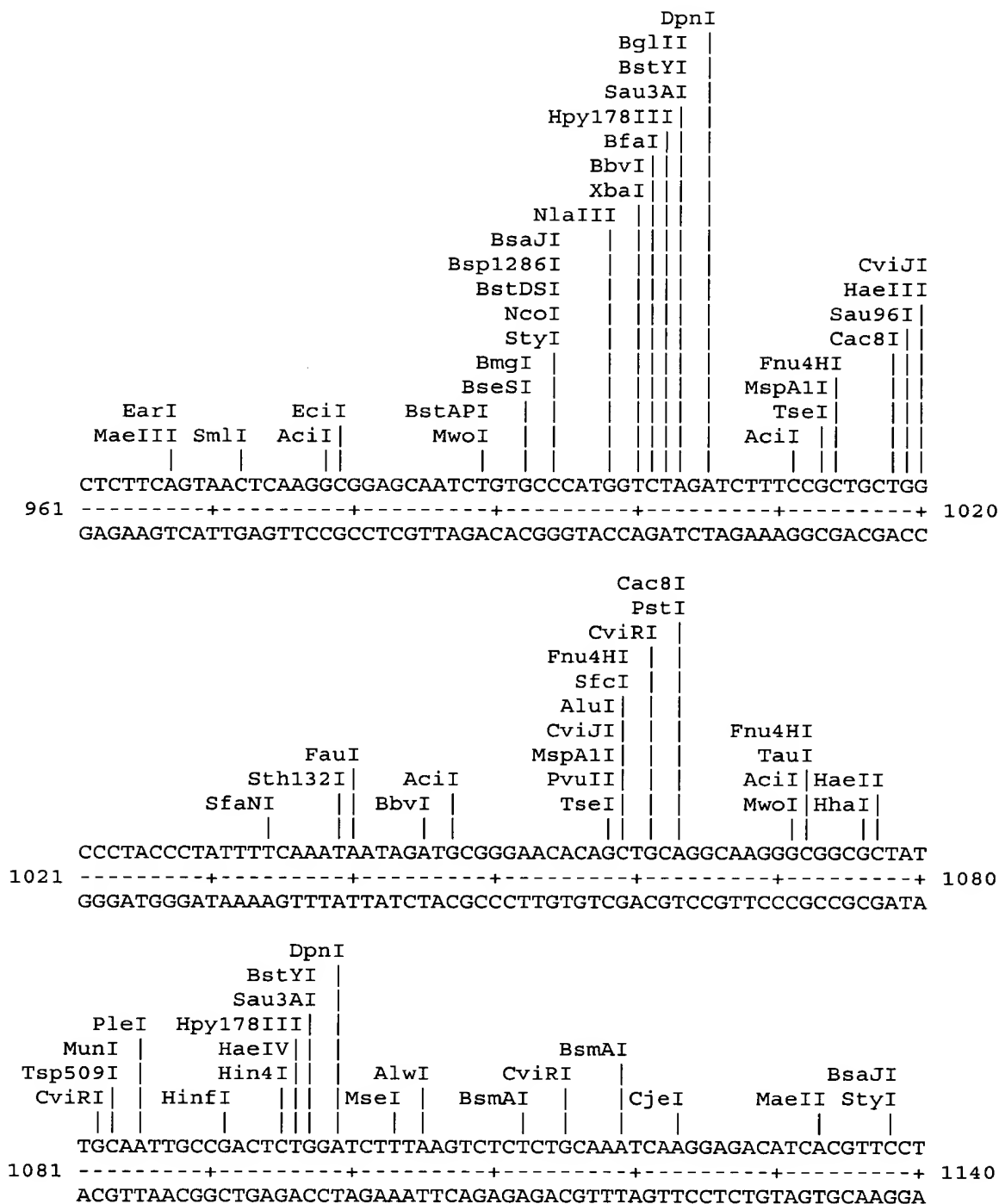


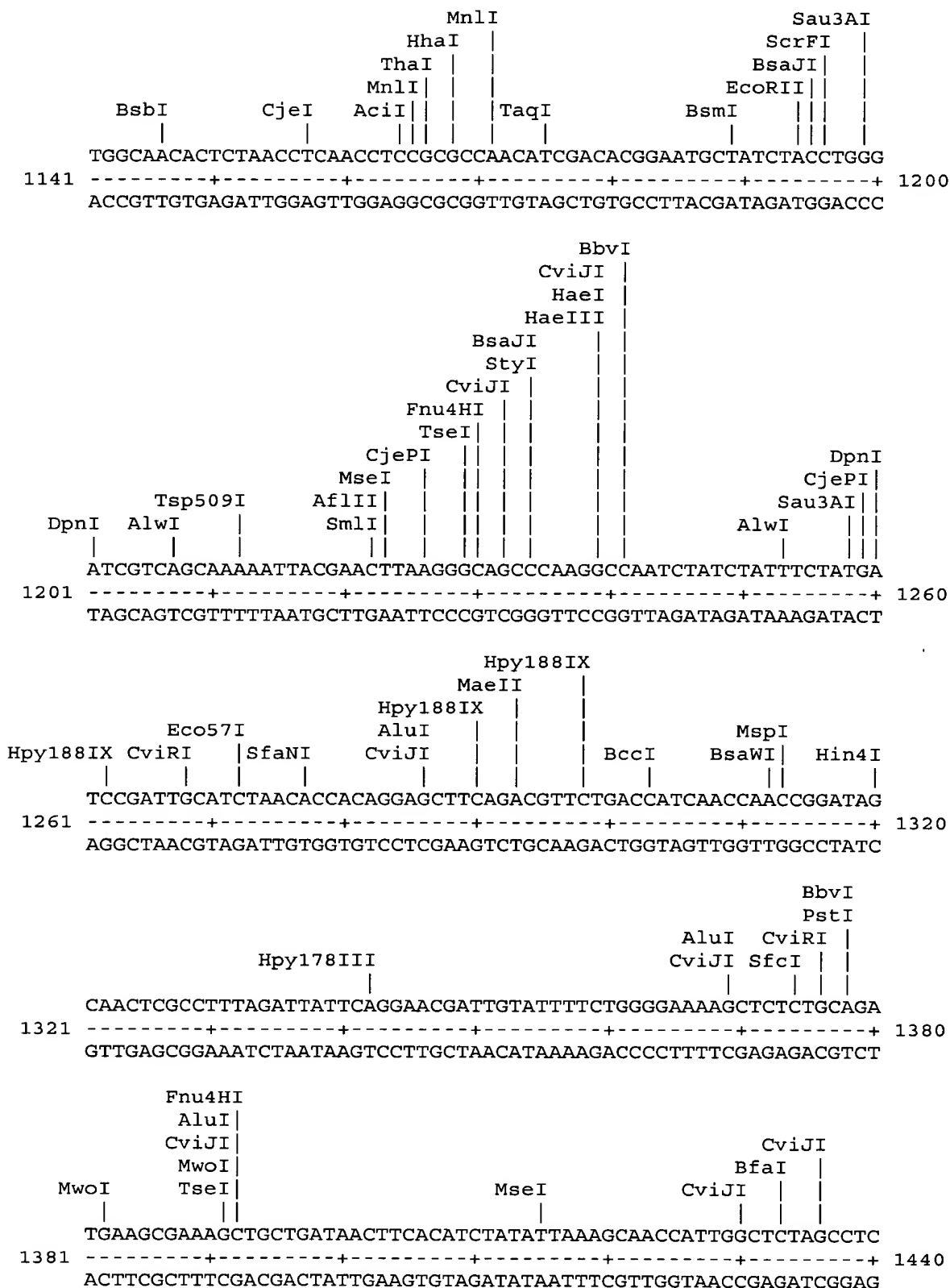
Fig. 8 E





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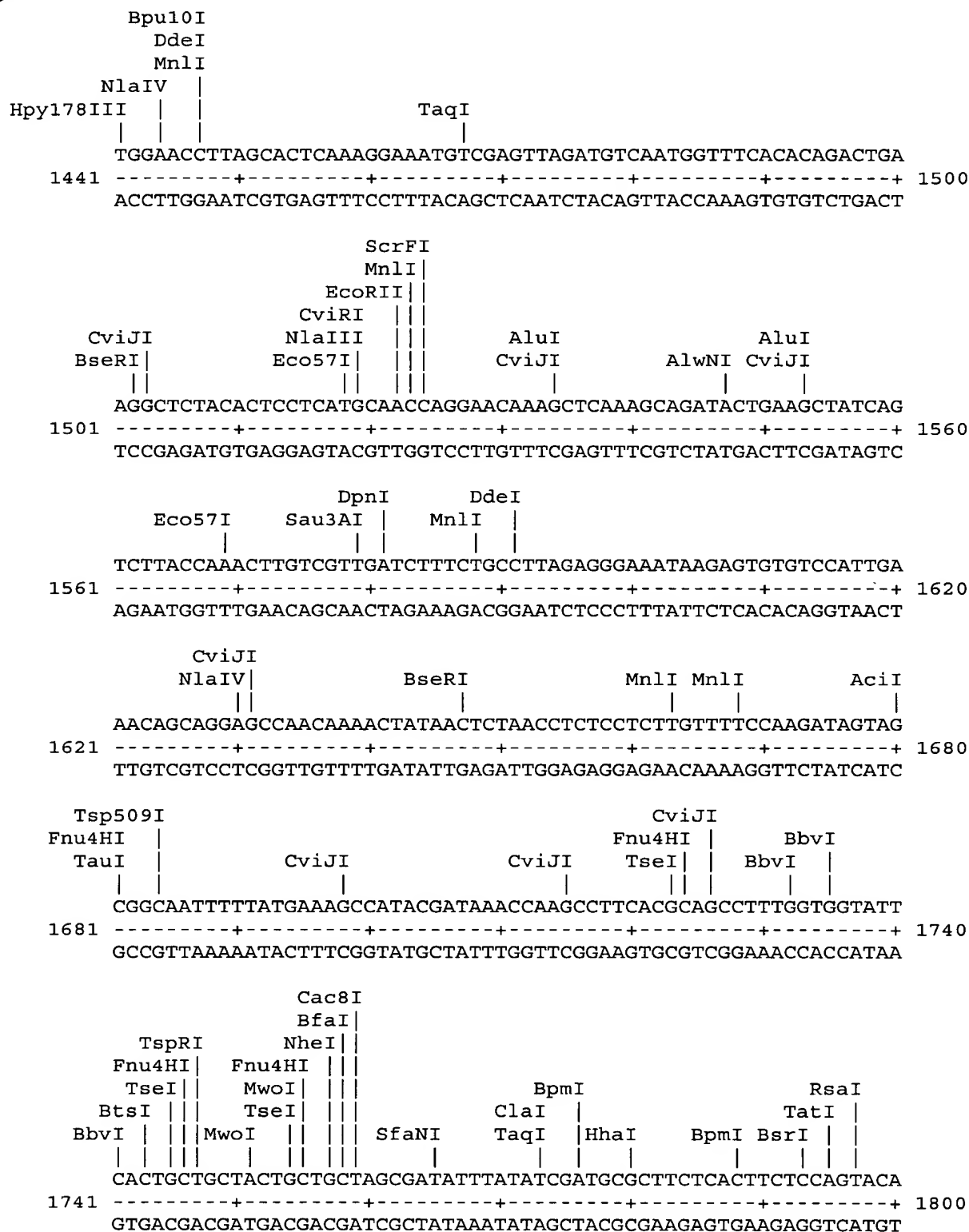
Fig. 8 F





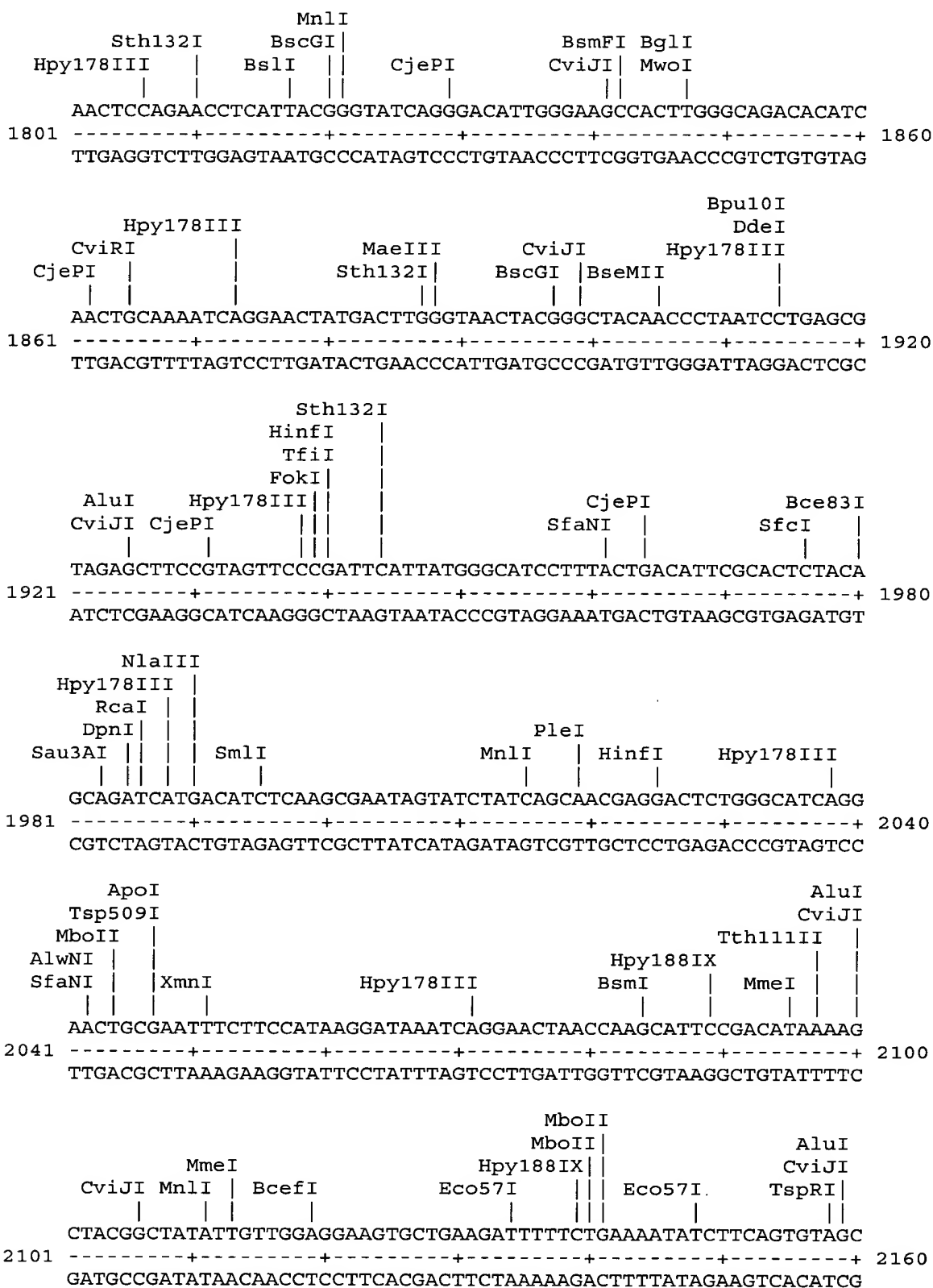
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Fig. 8 G



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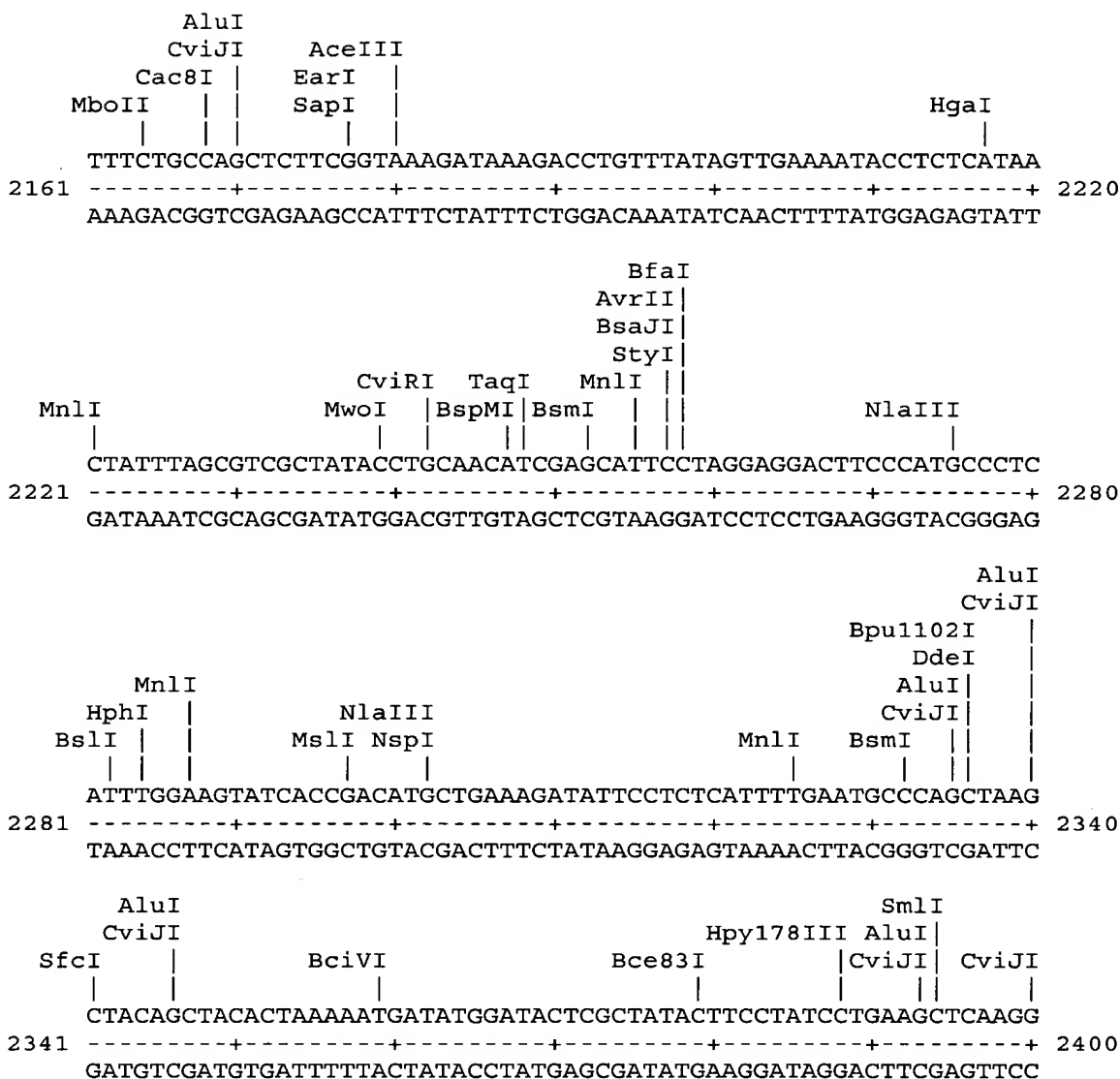
Fig. 8 H





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Fig. 8 I





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Fig. 8 J

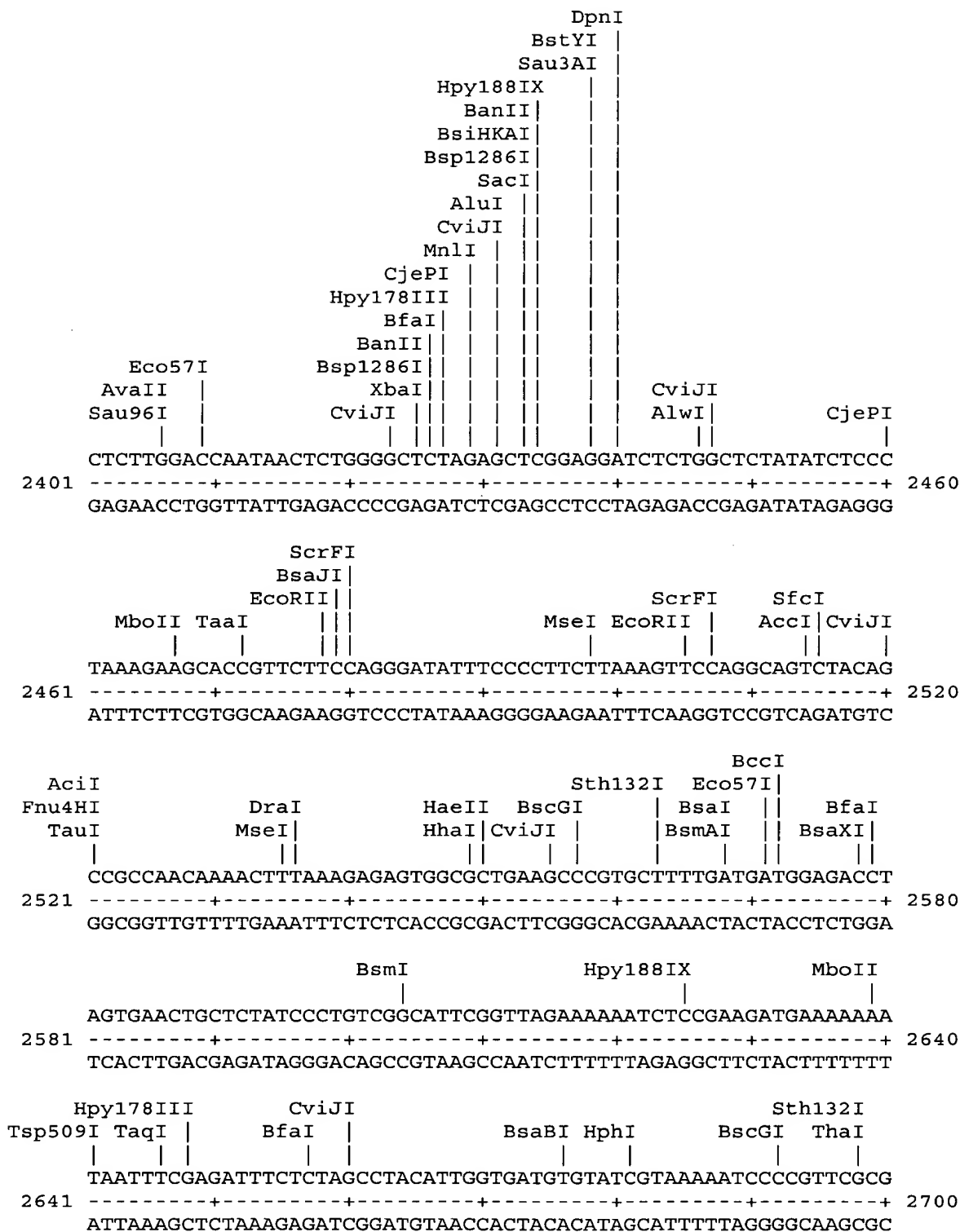
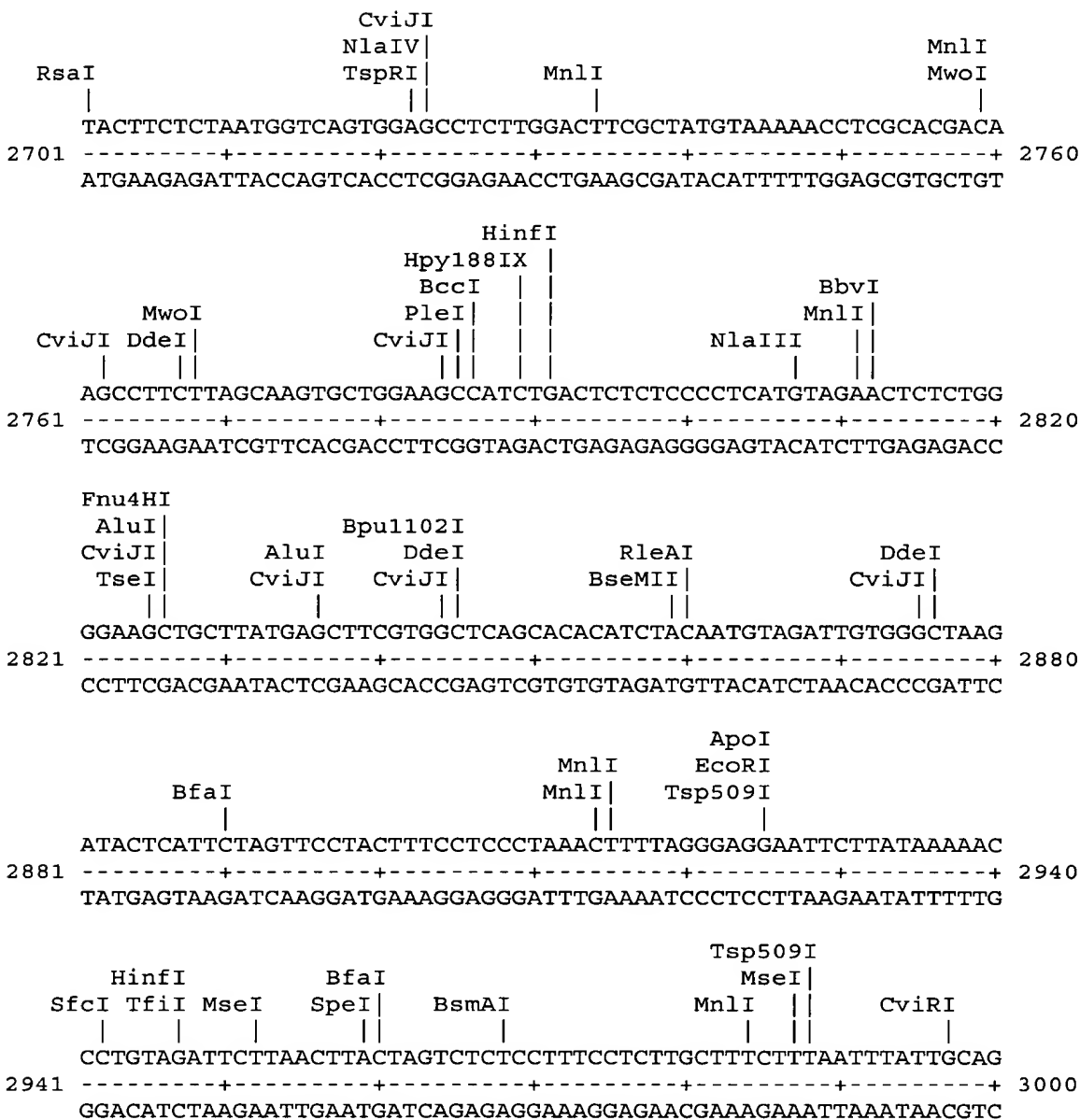




Fig. 8 K

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REPLACEMENT SHEET  
Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128



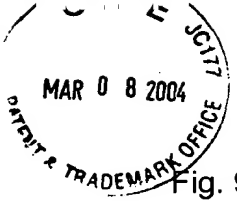


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Figure 9 A: Nucleotide and amino acid sequence of CPN100708

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ataaagtttt ttatatgaac aaaactttga cttcattggc agacacttcg accttaacag 60
accaattttg ttgtcatccc tataaaaatc aggaattttc atg ctc tcc tca cta 115
                                     Met Leu Ser Ser Leu
                                     1 5
atc cgt gat tca ttt ccc ctt ctt att tta ctt ccc aca ttc cta gcg 163
Ile Arg Asp Ser Phe Pro Leu Leu Ile Leu Leu Pro Thr Phe Leu Ala
                10                15                20
gca tta gga gcc tcc gta gct ggc ggc gtt atg gga acc tat atc gtt 211
Ala Leu Gly Ala Ser Val Ala Gly Gly Val Met Gly Thr Tyr Ile Val
                25                30                35
gta aaa cgt att gtt tca att agt gga agt ata tct cat gca att cta 259
Val Lys Arg Ile Val Ser Ile Ser Gly Ser Ile Ser His Ala Ile Leu
                40                45                50
gga gga att ggc ctc acc cta tgg ata caa tat aag ctt cat ctc tct 307
Gly Gly Ile Gly Leu Thr Leu Trp Ile Gln Tyr Lys Leu His Leu Ser
                55                60                65
ttt ttc cct atg tat gga gct att gta gga gct att ttt cta gct ctt 355
Phe Phe Pro Met Tyr Gly Ala Ile Val Gly Ala Ile Phe Leu Ala Leu
                70                75                80                85
tgc atc ggc aag atc cac ctg aaa tac caa gaa agg gaa gac tct ttg 403
Cys Ile Gly Lys Ile His Leu Lys Tyr Gln Glu Arg Glu Asp Ser Leu
                90                95                100
att gcg atg att tgg tct gtg ggc atg gca att gga att ata ttc att 451
Ile Ala Met Ile Trp Ser Val Gly Met Ala Ile Gly Ile Ile Phe Ile
                105                110                115
tcc agg ctt ccc acc ttt aat gga gag ctc atc aat ttt cta ttt ggg 499
Ser Arg Leu Pro Thr Phe Asn Gly Glu Leu Ile Asn Phe Leu Phe Gly
                120                125                130
aac att ctc tgg gtc acc cct tca gac ctc tat agc tta gga atc ttt 547
Asn Ile Leu Trp Val Thr Pro Ser Asp Leu Tyr Ser Leu Gly Ile Phe
                135                140                145
gat ctt ctt gtt tta gga att gtg gtc ctt tgc cac acc cgg ttc ctt 595
Asp Leu Leu Val Leu Gly Ile Val Val Leu Cys His Thr Arg Phe Leu
                150                155                160                165
gct ctt tgc ttt gat gag agg tac acg gct tta aac cat tgt tct gta 643
Ala Leu Cys Phe Asp Glu Arg Tyr Thr Ala Leu Asn His Cys Ser Val
                170                175                180
cag ctg tgg tat ttc cta ctt ctt gtt ctg aca gca atc acg att gtg 691
Gln Leu Trp Tyr Phe Leu Leu Leu Val Leu Thr Ala Ile Thr Ile Val
                185                190                195
```





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Fig. 9 B

atg ttg att tat gtg atg gga acg att ctg atg ctt agc atg ctc gtc	739
Met Leu Ile Tyr Val Met Gly Thr Ile Leu Met Leu Ser Met Leu Val	
200 205 210	
tta cct gtt gct ata gcg tgt aga ttt tcg tac aag atg aca cga att	787
Leu Pro Val Ala Ile Ala Cys Arg Phe Ser Tyr Lys Met Thr Arg Ile	
215 220 225	
atg ttc atc tcg gtc ctc ttg aat atc tta tgt tct ttt tct gga att	835
Met Phe Ile Ser Val Leu Leu Asn Ile Leu Cys Ser Phe Ser Gly Ile	
230 235 240 245	
tgc atc gcc tac tgt tta gat ttc cca gta ggt cct acg ata tca ttg	883
Cys Ile Ala Tyr Cys Leu Asp Phe Pro Val Gly Pro Thr Ile Ser Leu	
250 255 260	
ctg atg ggg tta ggt tat aca gcg agt ctt tgt gtg aag aag cgg tac	931
Leu Met Gly Leu Gly Tyr Thr Ala Ser Leu Cys Val Lys Lys Arg Tyr	
265 270 275	
aat ccg tcg acg cct tct cct gta agt cct gaa atc aat aca aat gta	979
Asn Pro Ser Thr Pro Ser Pro Val Ser Pro Glu Ile Asn Thr Asn Val	
280 285 290	
tagctaggga agcgcttttg gaagcttttg aggcattctt cctgttcgtc aggaagaaga	1039
tcacaaattt tatttaaagc taccagcata tctttctttt caaaatctgg ctgatgagag	1099
t	1100



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Figure 10 A: Restriction enzyme analysis of CPN100708

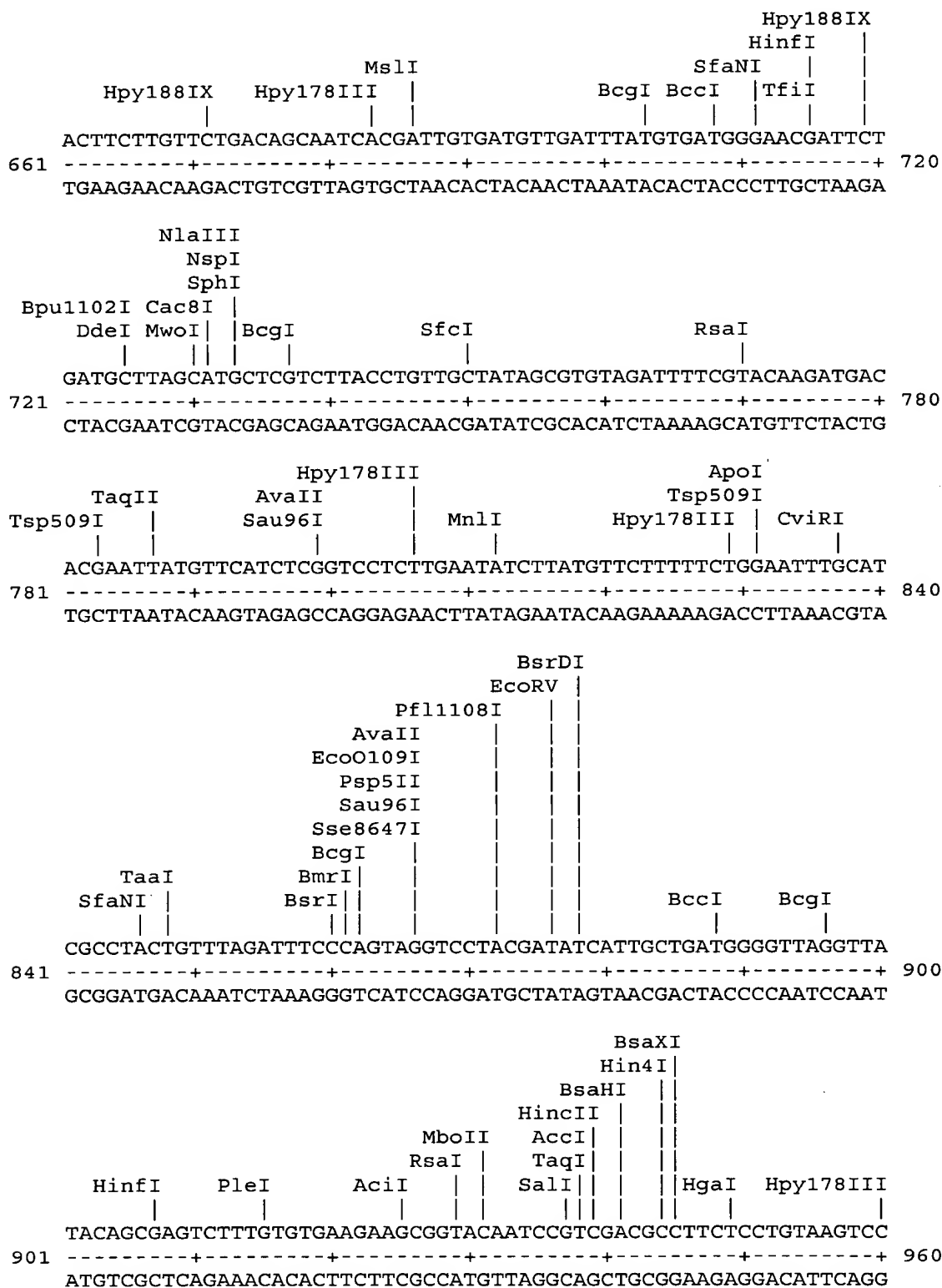


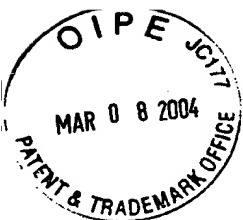




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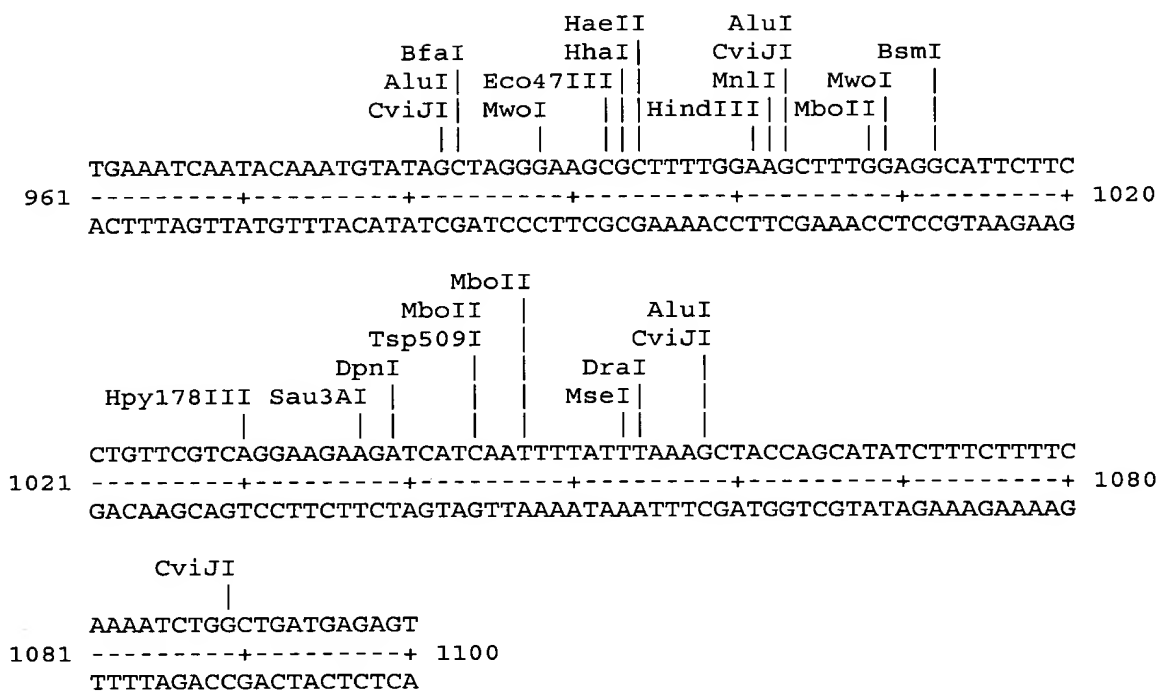
Fig. 10 C





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Fig. 10 D



ANNOTATED SHEET SHOWING CHANGES  
Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF



Fig. 1 B (cont.)

aca gca ggc gct cgc ata gca aat aac aca ggt tat gtt aga ttc cta	739
Thr Ala Gly Ala Arg Ile Ala Asn Asn Thr Gly Tyr Val Arg Phe Leu	
200 205 210	
tct aac ata gcg tct acg tca gga ggc gct atc gat gat gaa ggc acg	787
Ser Asn Ile Ala Ser Thr Ser Gly Gly Ala Ile Asp Asp Glu Gly Thr	
215 220 225	
tcg ata cta tcg aac aac aaa ttt cta tat ttt gaa ggg aat gca gcg	835
Ser Ile Leu Ser Asn Asn Lys Phe Leu Tyr Phe Glu Gly Asn Ala Ala	
230 235 240 245	
aaa act act ggc ggt gcg atc tgc aac acc aag gcg agt gga tct cct	883
Lys Thr Thr Gly Gly Ala Ile Cys Asn Thr Lys Ala Ser Gly Ser Pro	
250 255 260	
gaa ctg ata atc tct aac aat aag act ctg atc ttt gct tca aac gta	931
Glu Leu Ile Ile Ser Asn Asn Lys Thr Leu Ile Phe Ala Ser Asn Val	
265 270 275	
gca gaa aca agc ggt ggc gcc atc cat gct aaa aag cta gcc ctt tcc	979
Ala Glu Thr Ser Gly Gly Ala Ile His Ala Lys Lys Leu Ala Leu Ser	
280 285 290	
tct gga ggc ttt aca gag ttt cta cga aat aat gtc tca tca gca act	1027
Ser Gly Gly Phe Thr Glu Phe Leu Arg Asn Asn Val Ser Ser Ala Thr	
295 300 305	
cct aag ggg ggt gct atc agc atc gat gcc tca gga gag ctc agt ctt	1075
Pro Lys Gly Gly Ala Ile Ser Ile Asp Ala Ser Gly Glu Leu Ser Leu	
310 315 320 325	
tct gca gag aca gga aac att acc ttt gta aga aat acc ctt aca aca	1123
Ser Ala Glu Thr Gly Asn Ile Thr Phe Val Arg Asn Thr Leu Thr Thr	
330 335 340	
acc gga agt acc gat act cct aaa cgt aat gcg atc aac ata gga agt	1171
Thr Gly Ser Thr Asp Thr Pro Lys Arg Asn Ala Ile Asn Ile Gly Ser	
345 350 355	
aac ggg aaa ttc acg gaa tta cgg gct gct aaa aat cat aca att ttc	1219
Asn Gly Lys Phe Thr Glu Leu Arg Ala Ala Lys Asn His Thr Ile Phe	
360 365 370	
ttc tat gat ccc atc act tca gaa gga acc tca tca gac gta ttg aag	1267
Phe Tyr Asp Pro Ile Thr Ser Glu Gly Thr Ser Ser Asp Val Leu Lys	
375 380 385	
ata aat aac ggc tct gcg gga gct ctc aat cca tat caa gga acg att	1315
Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro Tyr Gln Gly Thr Ile	
390 395 400 405	
cta ttt tct gga gaa acc cta aca gca gat gaa ctt aaa gtt gct gac	1363
Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu Leu Lys Val Ala Asp	
410 415 420	

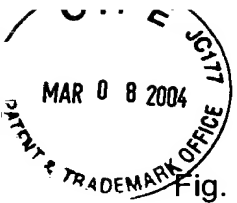


Fig. 1 C (cont.)

aat tta aaa tct tca ttc acg cag cca gtc tcc cta tcc gga gga aag	1411
Asn Leu Lys Ser Ser Phe Thr Gln Pro Val Ser Leu Ser Gly Gly Lys	
425 430 435	
tta ttg cta caa aag gga gtc act tta gag agc acg agc ttc tct caa	1459
Leu Leu Leu Gln Lys Gly Val Thr Leu Glu Ser Thr Ser Phe Ser Gln	
440 445 450	
gag gcc ggt tct ctc ctc ggc atg gat tca gga acg aca tta tca act	1507
Glu Ala Gly Ser Leu Leu Gly Met Asp Ser Gly Thr Thr Leu Ser Thr	
455 460 465	
aca gct ggg agt att aca atc acg aac cta gga atc aat gtt gac tcc	1555
Thr Ala Gly Ser Ile Thr Ile Thr Asn Leu Gly Ile Asn Val Asp Ser	
470 475 480 485	
tta ggt ctt aag cag ccc gtc agc cta aca gca aaa ggt gct tca aat	1603
Leu Gly Leu Lys Gln Pro Val Ser Leu Thr Ala Lys Gly Ala Ser Asn	
490 495 500	
aaa gtg atc gta tct ggg aag ctc aac ctg att gat att gaa ggg aac	1651
Lys Val Ile Val Ser Gly Lys Leu Asn Leu Ile Asp Ile Glu Gly Asn	
505 510 515	
att tat gaa agt cat atg ttc agc cat gac cag ctc ttc tct cta tta	1699
Ile Tyr Glu Ser His Met Phe Ser His Asp Gln Leu Phe Ser Leu Leu	
520 525 530	
aaa atc acg gtt gat gct gat gtt gat act aac gtt gac atc agc agc	1747
Lys Ile Thr Val Asp Ala Asp Val Asp Thr Asn Val Asp Ile Ser Ser	
535 540 545	
ctt atc cct gtt cct gct gag gat cct aat tca gaa tac gga ttc caa	1795
Leu Ile Pro Val Pro Ala Glu Asp Pro Asn Ser Glu Tyr Gly Phe Gln	
550 555 560 565	
gga caa tgg aat gtt aat tgg act acg gat aca gct aca aat aca aaa	1843
Gly Gln Trp Asn Val Asn Trp Thr Thr Asp Thr Ala Thr Asn Thr Lys	
570 575 580	
gag gcc acg gca act tgg acc aaa aca gga ttt gtt ccc agc ccc gaa	1891
Glu Ala Thr Ala Thr Trp Thr Lys Thr Gly Phe Val Pro Ser Pro Glu	
585 590 595	
aga aaa tct gcg tta gta tgc aat acc cta tgg gga gtc ttt act gac	1939
Arg Lys Ser Ala Leu Val Cys Asn Thr Leu Trp Gly Val Phe Thr Asp	
600 605 610	
att cgc tct ctg caa cag ctt gta gag atc ggc gca act ggt atg gaa	1987
Ile Arg Ser Leu Gln Gln Leu Val Glu Ile Gly Ala Thr Gly Met Glu	
615 620 625	
cac aaa caa ggt ttc tgg gtt tcc tcc atg acg aac ttc ctg cat aag	2035
His Lys Gln Gly Phe Trp Val Ser Ser Met Thr Asn Phe Leu His Lys	
630 635 640 645	





Fig. 1 D (cont.)

act gga gat gaa aat cgc aaa ggc ttc cgt cat acc tct gga ggc tac	2083
Thr Gly Asp Glu Asn Arg Lys Gly Phe Arg His Thr Ser Gly Gly Tyr	
650 655 660	
gtc atc ggt gga agt gct cac act cct aaa gac gac cta ttt acc ttt	2131
Val Ile Gly Gly Ser Ala His Thr Pro Lys Asp Asp Leu Phe Thr Phe	
665 670 675	
gcg ttc tgc cat ctc ttt gct aga gac aaa gat tgt ttt atc gct cac	2179
Ala Phe Cys His Leu Phe Ala Arg Asp Lys Asp Cys Phe Ile Ala His	
680 685 690	
aac aac tct aga acc tac ggt gga act tta ttc ttc aag cac tct cat	2227
Asn Asn Ser Arg Thr Tyr Gly Gly Thr Leu Phe Phe Lys His Ser His	
695 700 705	
acc cta caa ccc caa aac tat ttg aga tta gga aga gca aag ttt tct	2275
Thr Leu Gln Pro Gln Asn Tyr Leu Arg Leu Gly Arg Ala Lys Phe Ser	
710 715 720 725	
gaa tca gct ata gaa aaa ttc cct agg gaa att ccc cta gcc ttg gat	2323
Glu Ser Ala Ile Glu Lys Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp	
730 735 740	
gtc caa gtt tcg ttc agc cat tca gac aac cgt atg gaa acg cac tat	2371
Val Gln Val Ser Phe Ser His Ser Asp Asn Arg Met Glu Thr His Tyr	
745 750 755	
acc tca ttg cca gaa tcc gaa ggt tct tgg agc aac gag tgt ata gct	2419
Thr Ser Leu Pro Glu Ser Glu Gly Ser Trp Ser Asn Glu Cys Ile Ala	
760 765 770	
ggg ggt atc ggc cta gac ctt cct ttt gtt ctt tcc aac cca cat cct	2467
Gly Gly Ile Gly Leu Asp Leu Pro Phe Val Leu Ser Asn Pro His Pro	
775 780 785	
ctt ttc aag acc ttc att cca cag atg aaa gtc gaa atg gtt tat gta	2515
Leu Phe Lys Thr Phe Ile Pro Gln Met Lys Val Glu Met Val Tyr Val	
790 795 800 805	
tca caa aat agc ttc ttc gaa agc tct agt gat ggc cgt ggt ttt agt	2563
Ser Gln Asn Ser Phe Phe Glu Ser Ser Ser Asp Gly Arg Gly Phe Ser	
810 815 820	
att gga agg ctg ctt aac ctc tcg att cct gtg ggt gcg aaa ttc gtg	2611
Ile Gly Arg Leu Leu Asn Leu Ser Ile Pro Val Gly Ala Lys Phe Val	
825 830 835	
cag ggg gat atc gga gat tcc tac acc tat gat ctc tca gga ttc ttt	2659
Gln Gly Asp Ile Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe	
840 845 850	
gtt tcc gat gtc tat cgt aac aat ccc caa tct aca gcg act ctt gtg	2707
Val Ser Asp Val Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val	
855 860 865	

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Fig. 1 E (con't)

atg agc cca gac tct tgg aaa att cgc ggt ggc aat ctt tca aga cag	2755
Met Ser Pro Asp Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln	
870 875 880 885	
gca ttt tta ctg agg ggt agc aac aac tac gtc tac aac tcc aat tgt	2803
Ala Phe Leu Leu Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys	
890 895 900	
gag ctc ttc gga cat tac gct atg gaa ctc cgt gga tct tca agg aac	2851
Glu Leu Phe Gly His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn	
905 910 915	
tac aat gta gat gtt ggt acc aaa ctc cga ttc tagattgcta aaactcccta	2904
Tyr Asn Val Asp Val Gly Thr Lys Leu Arg Phe	
920 925	
gttcttcttag ggagttttct catactttta gggaaatatt tgctat	2950

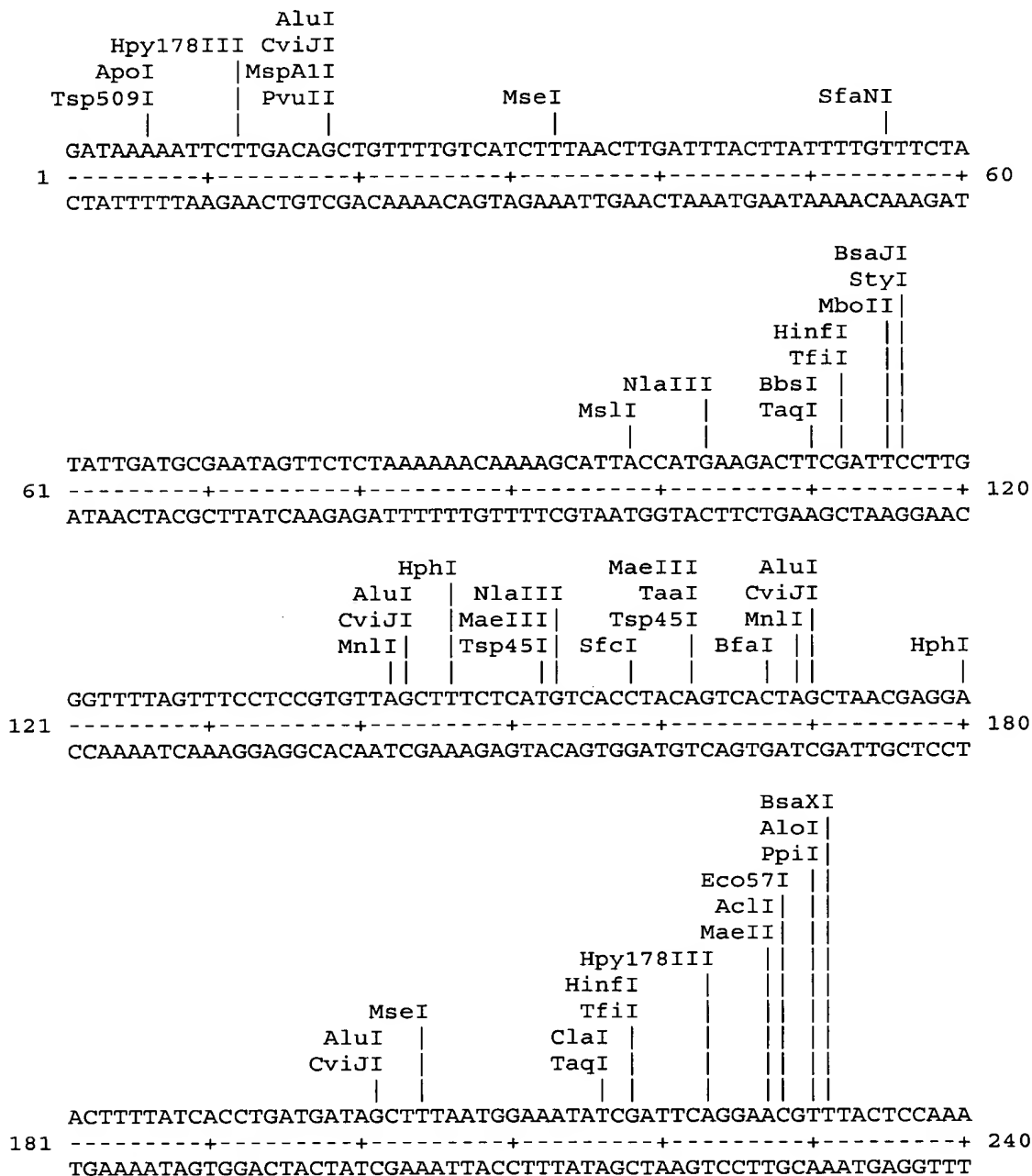


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ANNOTATED SHEET SHOWING CHANGES  
Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF

Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128

Figure 2 A: Restriction enzyme analysis of CPN100634



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Fig. 2 B (cont)

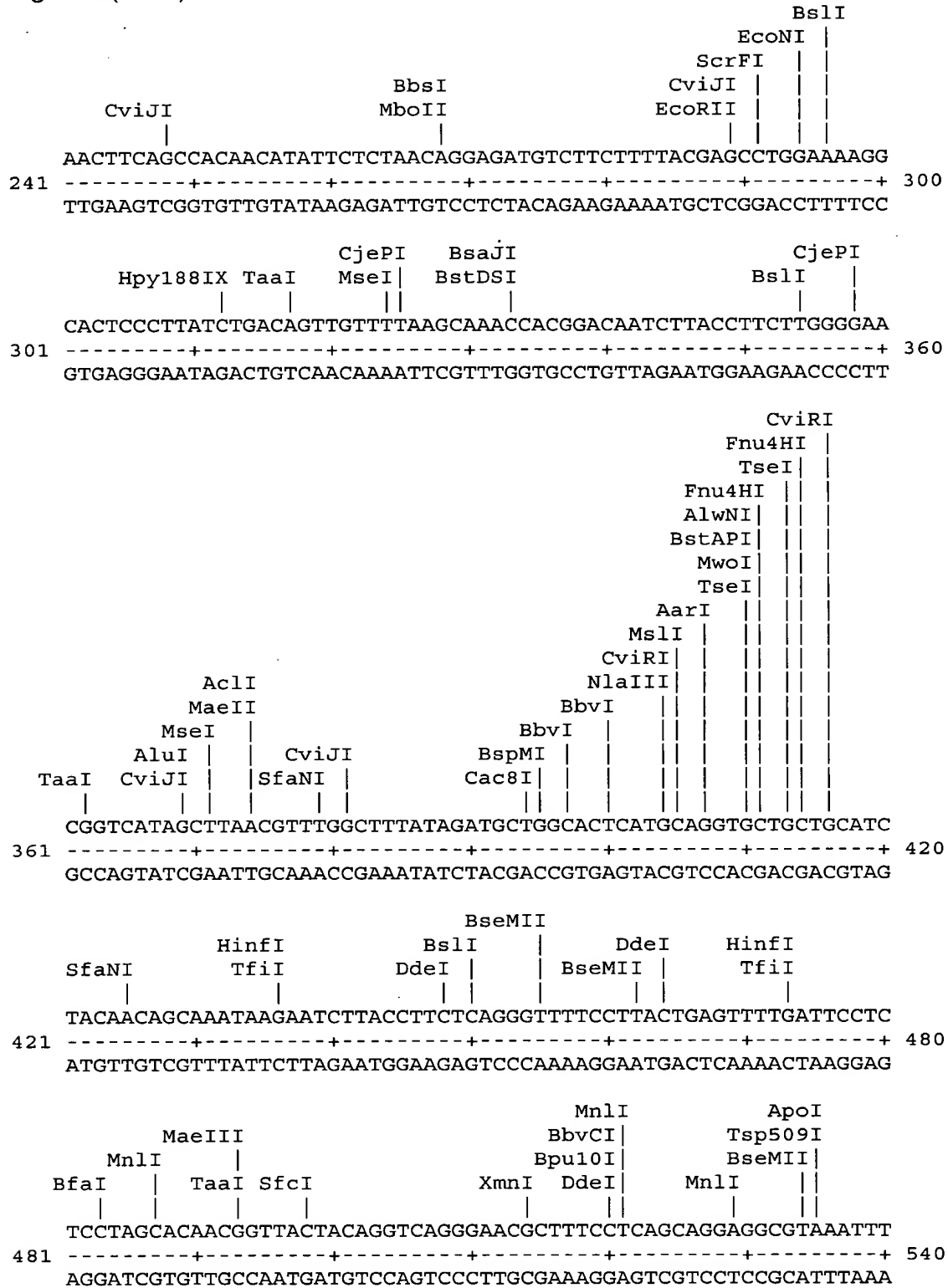
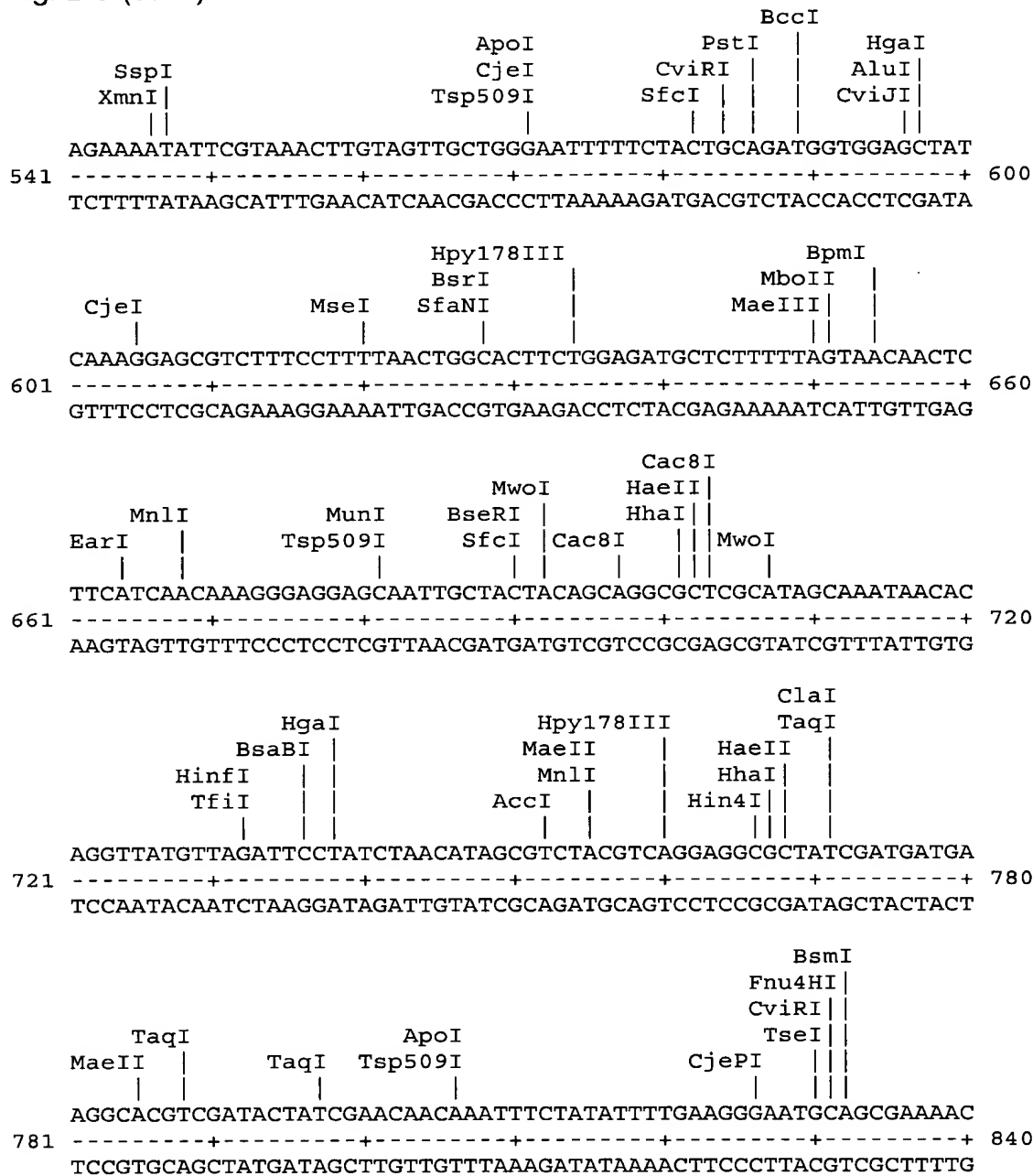


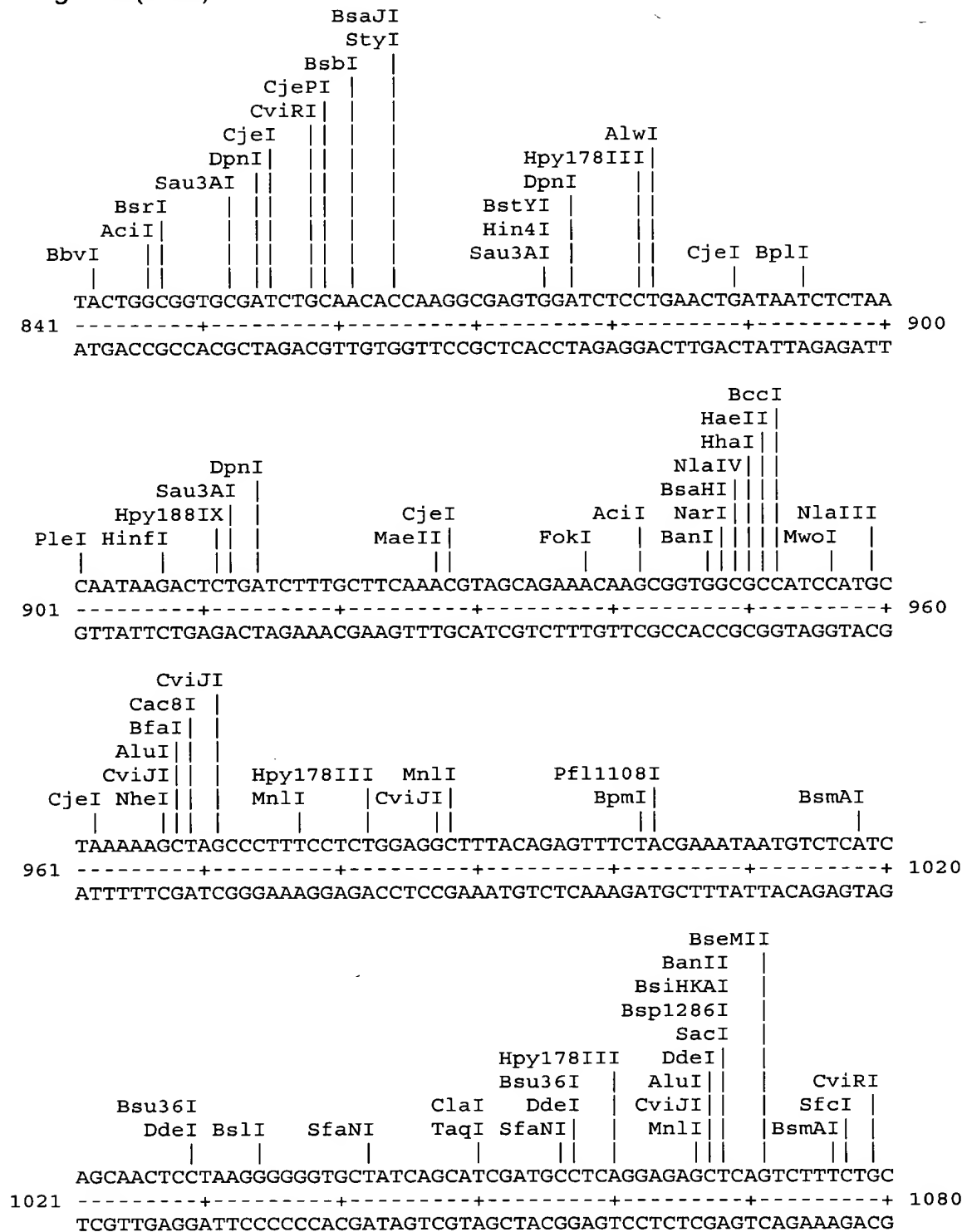


Fig. 2 C (cont)



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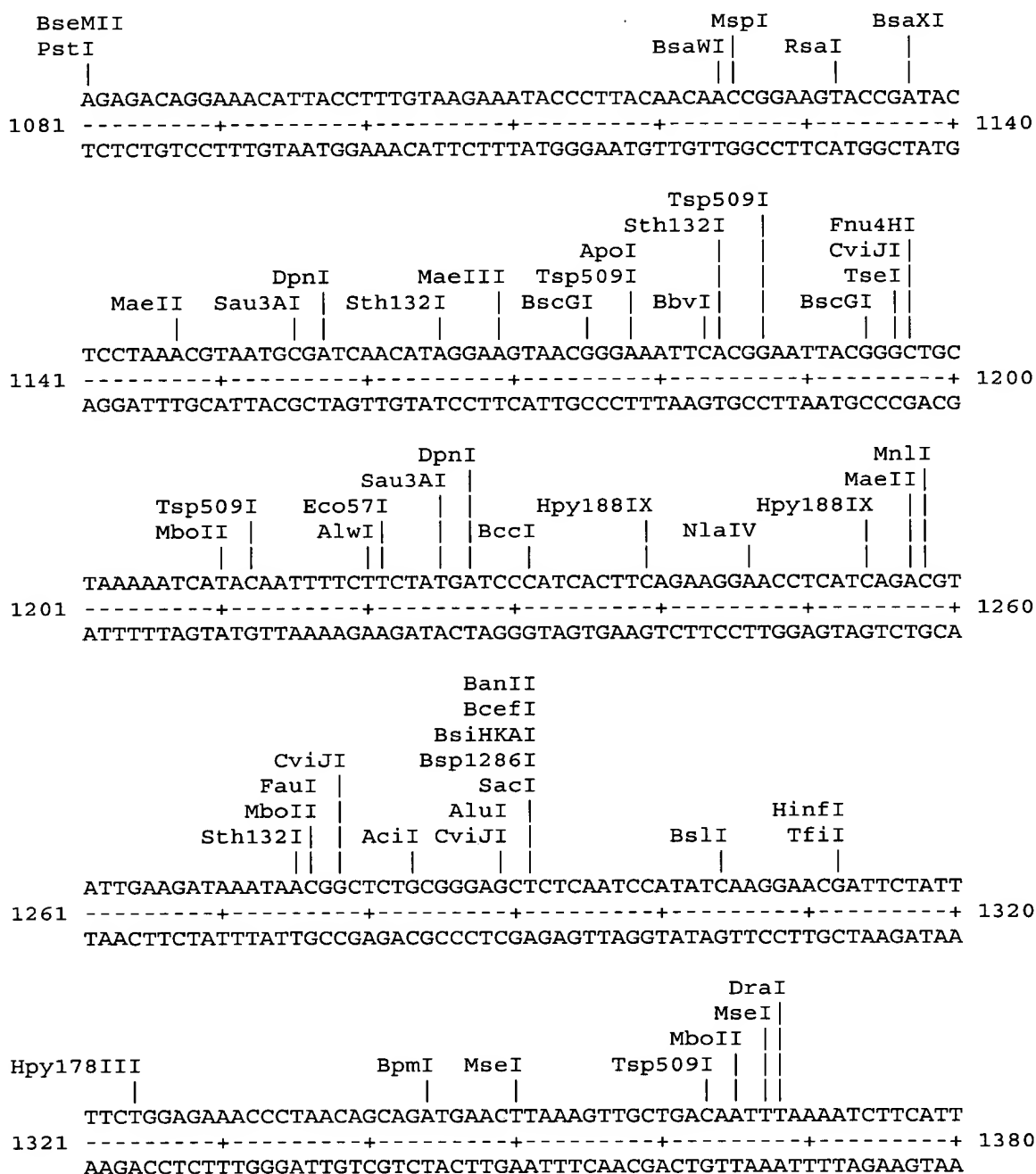
Fig. 2D (cont.)





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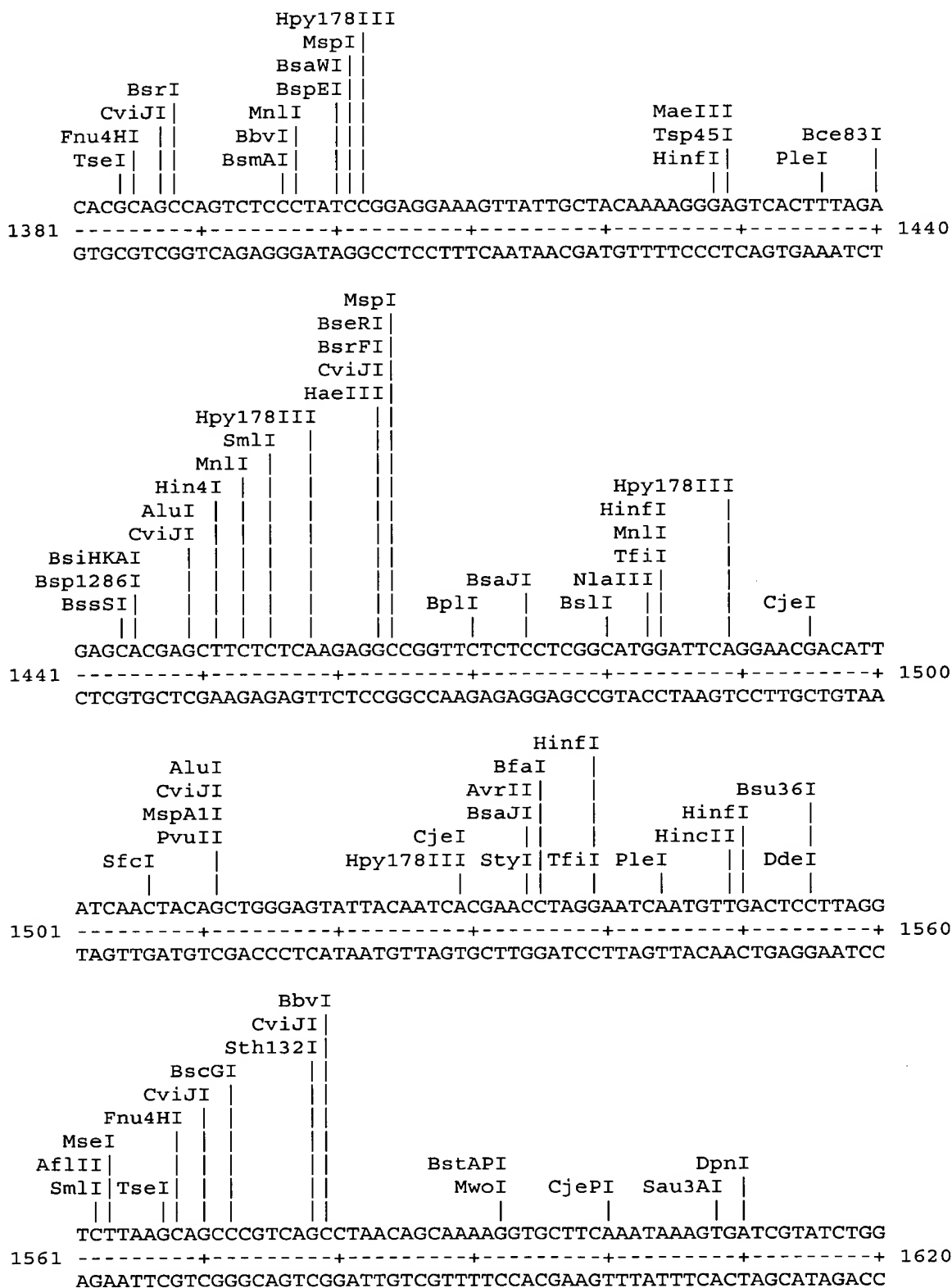
Fig. 2 E (cont)





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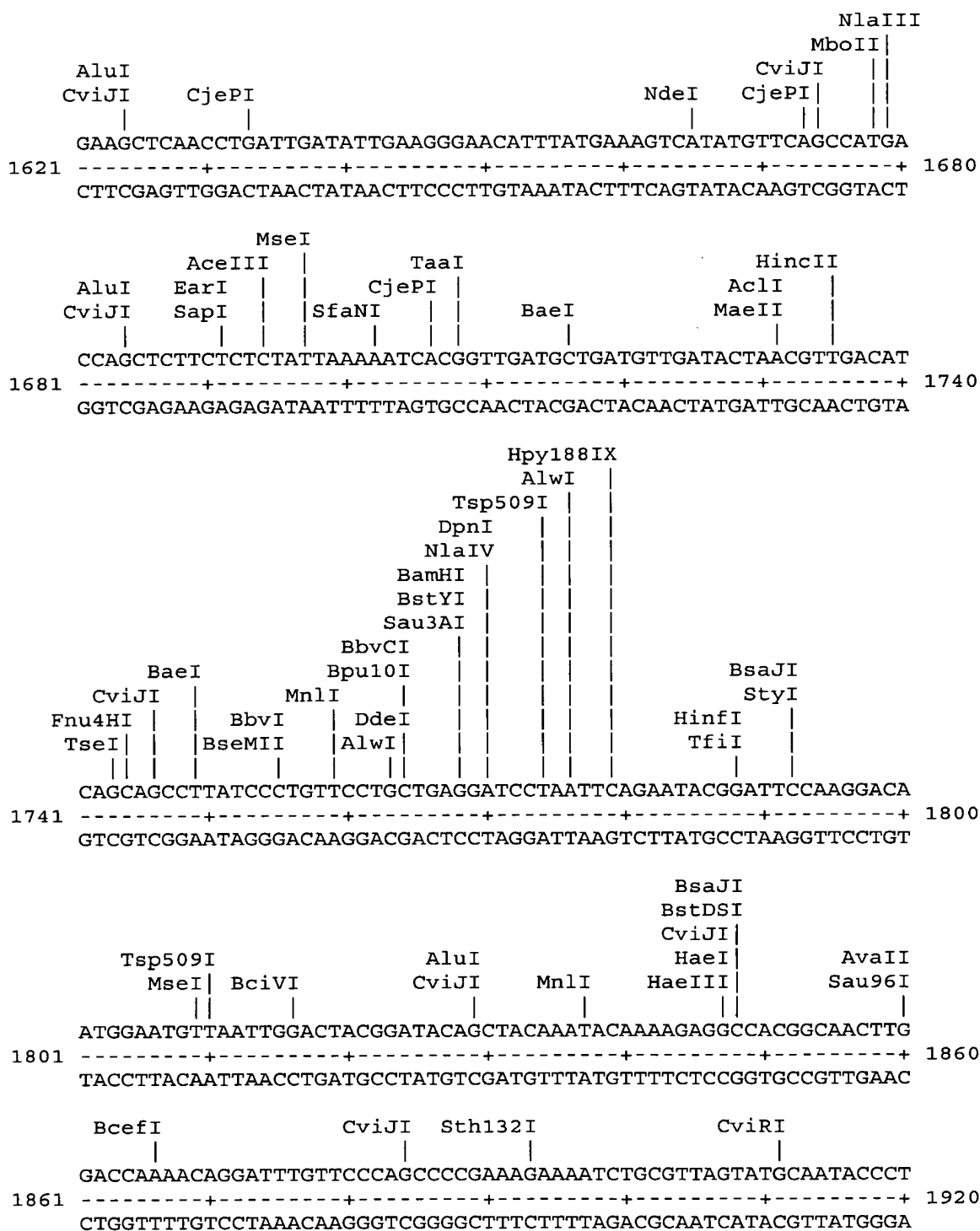
Fig. 2F (cont.)





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Fig. 2 G (cont)





[illegible]



Fig. 2 J (cont.)

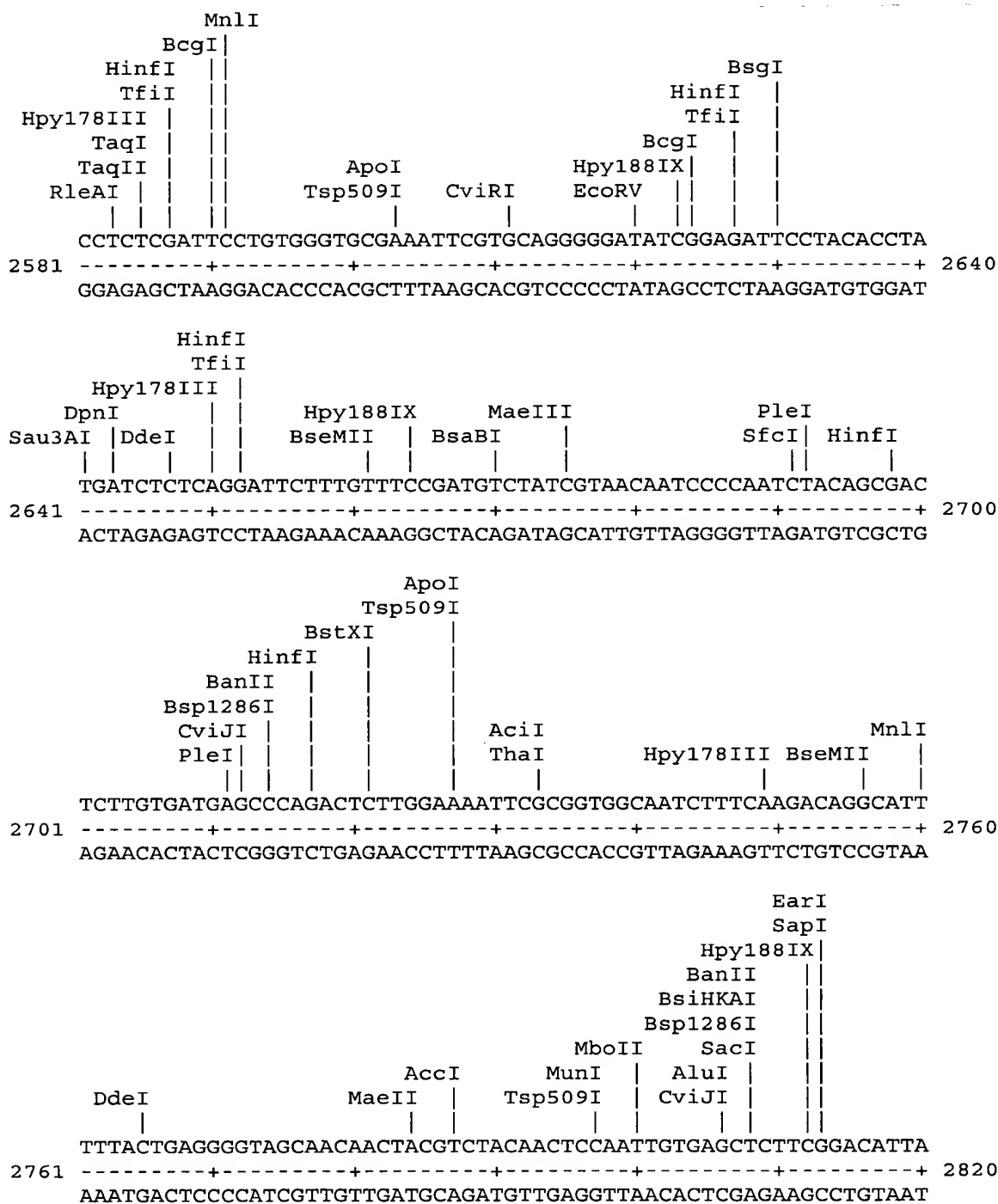




Fig. 2 K (cont)

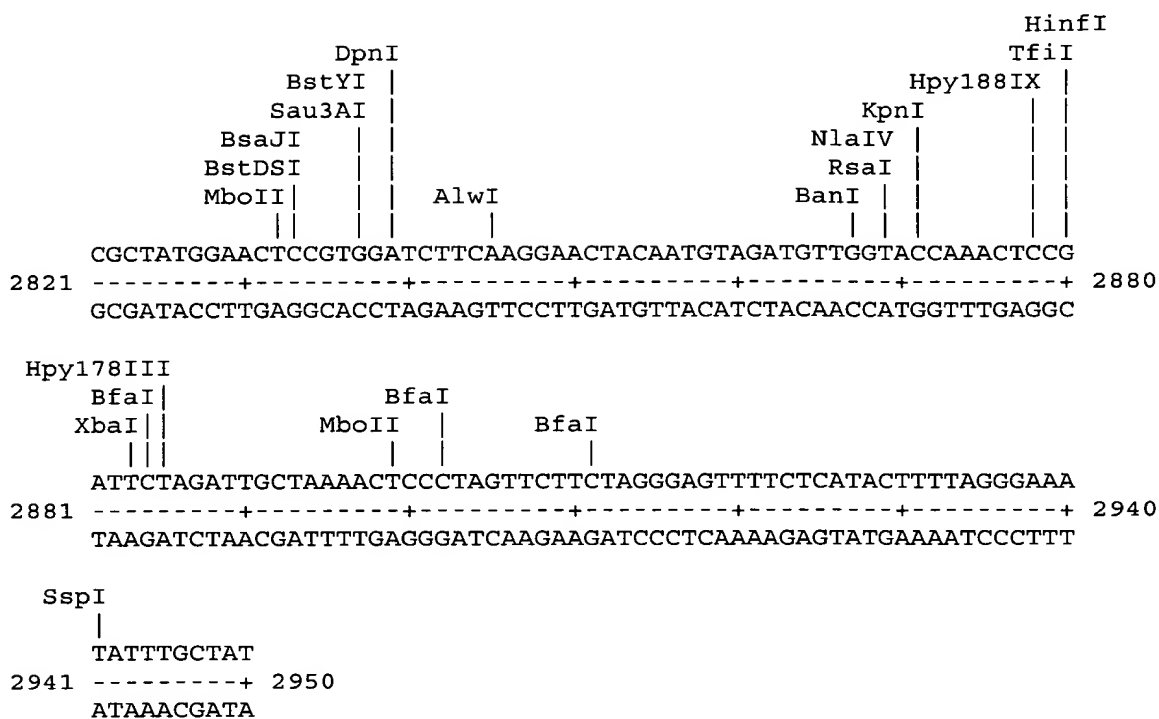




Figure 3 A: Nucleotide and deduced amino acid sequence of CPN100635

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agttaaagat gacaaaacag ctgtcaagaa tttttatctt gactctctga gttttctatt 60
ttatatgacg caagtaagaa ttttaataata aagtggggtt atg aaa tcg caa ttt 115
Met Lys Ser Gln Phe
1 5
tcc tgg tta gtg ctc tct tcg aca ttg gca tgt ttt act agt tgt tcc 163
Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys Phe Thr Ser Cys Ser
10 15 20
act gtt ttt gct gca act gct gaa aat ata ggc ccc tct gat agc ttt 211
Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly Pro Ser Asp Ser Phe
25 30 35
gac gga agt act aac aca ggc acc tat act cct aaa aat acg act act 259
Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro Lys Asn Thr Thr Thr
40 45 50
gga ata gac tat act ctg aca gga gat ata act ctg caa aac ctt ggg 307
Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly
Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly
55 60 65
gat tcg gca gct tta acg aag ggt tgt ttt tct gac act acg gaa tct 355
Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser Asp Thr Thr Glu Ser
Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser Asp Thr Thr Glu Ser
70 75 80 85
tta agc ttt gcc ggt aag ggg tac tca ctt tct ttt tta aat att aag 403
Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser Phe Leu Asn Ile Lys
Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser Phe Leu Asn Ile Lys
90 95 100
tct agt gct gaa ggc gca gcc ctt tct gtt aca act gat aaa aat ctg 451
Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr Thr Asp Lys Asn Leu
Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr Thr Asp Lys Asn Leu
105 110 115
tcg cta aca gga ttt tcg agt ctt act ttc tta gcg gcc cca tca tcg 499
Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser
Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser
120 125 130
gta atc aca acc ccc tca gga aaa ggt gca gtt aaa tgt gga ggg gat 547
Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val Lys Cys Gly Gly Asp
Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val Lys Cys Gly Gly Asp
135 140 145
ctt aca ttt gat aac aat gga act att tta ttt aaa caa gat tac tgt 595
Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys
Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys
150 155 160 165
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Fig. 3B (cont.)

gag gaa aat ggc gga gcc att tct acc aag aat ctt tct ttg aaa aac	643
Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn	
Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn	
170 175 180	
agc acg gga tcg att tct ttt gaa ggg aat aaa tcg agc gca aca ggg	691
Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly	
Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly	
185 190 195	
aaa aaa ggt ggg gct att tgt gct act ggt act gta gat att aca aat	739
Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn	
Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn	
200 205 210	
aat acg gct cct acc ctc ttc tcg aac aat att gct gaa gct gca ggt	787
Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly	
Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly	
215 220 225	
gga gct ata aat agc aca gga aac tgt aca att aca ggg aat acg tct	835
Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser	
Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser	
230 235 240 245	
ctt gta ttt tct gaa aat agt gtg aca gcg acc gca gga aat gga gga	883
Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly	
Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly	
250 255 260	
gct ctt tct gga gat gcc gat gtt acc ata tct ggg aat cag agt gta	931
Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser Gly Asn Gln Ser Val	
Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser Gly Asn Gln Ser Val	
265 270 275	
act ttc tca gga aac caa gct gta gct aat ggc gga gcc att tat gct	979
Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala	
Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala	
280 285 290	
aag aag ctt aca ctg gct tcc ggg ggg ggg ggg ggg aat ccc ttt tct	1027
Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly Gly Asn Pro Phe Ser	
Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly Gly Asn Pro Phe Ser	
295 300 305	
aac aat ata gtc caa ggt acc act gca ggt aat ggt gga gcc att tct	1075
Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn Gly Gly Ala Ile Ser	
Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn Gly Gly Ala Ile Ser	
310 315 320 325	
ata ctg gca gct gga gag tgt agt ctt ttc agc gaa gca ggg gac cat	1123
Ile Leu Ala Ala Gly Glu Cys Ser Leu Phe Ser Glu Ala Gly Asp His	
Ile Leu Ala Ala Gly Glu Cys Ser Leu Phe Ser Glu Ala Gly Asp His	
330 335 340	



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Fig. 3C (con't)

tac ctt aat ggg aat gcc att gtt gca act aca cca caa act aca aaa	1171
Tyr Leu Asn Gly Asn Ala Ile Val Ala Thr Thr Pro Gln Thr Thr Lys	
Tyr Leu Asn Gly Asn Ala Ile Val Ala Thr Thr Pro Gln Thr Thr Lys	
345 350 355	
aga aat tct att gac ata gga tct act ggc aaa gat cac gaa tta cgt	1219
Arg Asn Ser Ile Asp Ile Gly Ser Thr Gly Lys Asp His Glu Leu Arg	
Arg Asn Ser Ile Asp Ile Gly Ser Thr Gly Lys Asp His Glu Leu Arg	
360 365 370	
gca ata tct ggg cat agc atc ttt ttc tac gat ccg att act gct aat	1267
Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn	
Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn	
375 380 385	
acg gct gcg gat tct aca gat act tta aat ctc aat aag gct gat gca	1315
Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala	
Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala	
390 395 400 405	
ggg aat agt aca gat tat agt ggg tcg att gtt ttt tct ggt gaa aag	1363
Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val Phe Ser Gly Glu Lys	
Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val Phe Ser Gly Glu Lys	
410 415 420	
ctc tct gaa gat gaa gca aaa gtt gca gac aac ctc act tct acg ctg	1411
Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn Leu Thr Ser Thr Leu	
Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn Leu Thr Ser Thr Leu	
425 430 435	
aag cag cct gta act cta act gca gga aat tta gta ctt aaa cgt ggt	1459
Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu Val Leu Lys Arg Gly	
Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu Val Leu Lys Arg Gly	
440 445 450	
gtc act ctc gat acg aaa ggc ttt act cag acc gcg ggt tcc tct gtt	1507
Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr Ala Gly Ser Ser Val	
Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr Ala Gly Ser Ser Val	
455 460 465	
att atg gat gcg ggc aca acg tta aaa gca agt aca gag gag gtc act	1555
Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser Thr Glu Glu Val Thr	
Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser Thr Glu Glu Val Thr	
470 475 480 485	
tta aca ggt ctt tcc att cct gta gac tct tta ggc gag ggt aag aaa	1603
Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu Gly Glu Gly Lys Lys	
Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu Gly Glu Gly Lys Lys	
490 495 500	
gtt gta att gct gct tct gca gca agt aaa aat gta gcc ctt agt ggt	1651
Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn Val Ala Leu Ser Gly	
Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn Val Ala Leu Ser Gly	
505 510 515	





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Fig. 3 D (con't)

ccg att ctt ctt ttg gat aac caa ggg aat gct tat gaa aat cac gac	1699
Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala Tyr Glu Asn His Asp	
Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala Tyr Glu Asn His Asp	
520 525 530	
tta gga aaa act caa gac ttt tca ttt gtg cag ctc tct gct ctg ggt	1747
Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln Leu Ser Ala Leu Gly	
Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln Leu Ser Ala Leu Gly	
535 540 545	
act gca aca act aca gat gtt cca gcg gtt cct aca gta gca act cct	1795
Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro Thr Val Ala Thr Pro	
Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro Thr Val Ala Thr Pro	
550 555 560 565	
acg cac tat ggg tat caa ggt act tgg gga atg act tgg gtt gat gat	1843
Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met Thr Trp Val Asp Asp	
Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met Thr Trp Val Asp Asp	
570 575 580	
acc gca agc act cca aag act aag aca gcg aca tta gct tgg acc aat	1891
Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn	
Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn	
585 590 595	
aca ggc tac ctt ccg aat cct gag cgt caa gga cct tta gtt cct aat	1939
Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn	
Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn	
600 605 610	
agc ctt tgg gga tct ttt tca gac atc caa gcg att caa ggt gtc ata	1987
Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala Ile Gln Gly Val Ile	
Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala Ile Gln Gly Val Ile	
615 620 625	
gag aga agt gct ttg act ctt tgt tca gat cga ggc ttc tgg gct gcg	2035
Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala	
Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala	
630 635 640 645	
gga gtc gcc aat ttc tta gat aaa gat aag aaa ggg gaa aaa cgc aaa	2083
Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys	
Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys	
650 655 660	
tac cgt cat aaa tct ggt gga tat gct atc gga ggt gca gcg caa act	2131
Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr	
Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr	
665 670 675	
tgt tct gaa aac tta att agc ttt gcc ttt tgc caa ctc ttt ggt agc	2179
Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser	
Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser	
680 685 690	



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Fig. 3 E (cont.)

gat	aaa	gat	ttc	tta	gtc	gct	aaa	aat	cat	act	gat	acc	tat	gca	gga	2227
Asp	Lys	Asp	Phe	Leu	Val	Ala	Lys	Asn	His	Thr	Asp	Thr	Tyr	Ala	Gly	
Asp	Lys	Asp	Phe	Leu	Val	Ala	Lys	Asn	His	Thr	Asp	Thr	Tyr	Ala	Gly	
	695						700				705					
gcc	ttc	tat	atc	caa	cac	att	aca	gaa	tgt	agt	ggg	ttc	ata	ggt	tgt	2275
Ala	Phe	Tyr	Ile	Gln	His	Ile	Thr	Glu	Cys	Ser	Gly	Phe	Ile	Gly	Cys	
Ala	Phe	Tyr	Ile	Gln	His	Ile	Thr	Glu	Cys	Ser	Gly	Phe	Ile	Gly	Cys	
	710					715				720					725	
ctc	tta	gat	aaa	ctt	cct	ggc	tct	tgg	agt	cat	aaa	ccc	ctc	gtt	tta	2323
Leu	Leu	Asp	Lys	Leu	Pro	Gly	Ser	Trp	Ser	His	Lys	Pro	Leu	Val	Leu	
Leu	Leu	Asp	Lys	Leu	Pro	Gly	Ser	Trp	Ser	His	Lys	Pro	Leu	Val	Leu	
				730					735						740	
gaa	ggg	cag	ctc	gct	tat	agc	cac	gtc	agt	aat	gat	ctg	aag	aca	aag	2371
Glu	Gly	Gln	Leu	Ala	Tyr	Ser	His	Val	Ser	Asn	Asp	Leu	Lys	Thr	Lys	
Glu	Gly	Gln	Leu	Ala	Tyr	Ser	His	Val	Ser	Asn	Asp	Leu	Lys	Thr	Lys	
			745					750						755		
tat	act	gcg	tat	cct	gag	gtg	aaa	ggg	tct	tgg	ggg	aat	aat	gct	ttt	2419
Tyr	Thr	Ala	Tyr	Pro	Glu	Val	Lys	Gly	Ser	Trp	Gly	Asn	Asn	Ala	Phe	
Tyr	Thr	Ala	Tyr	Pro	Glu	Val	Lys	Gly	Ser	Trp	Gly	Asn	Asn	Ala	Phe	
			760					765						770		
aac	atg	atg	ttg	gga	gct	tct	tct	cat	tct	tat	cct	gaa	tac	ctg	cat	2467
Asn	Met	Met	Leu	Gly	Ala	Ser	Ser	His	Ser	Tyr	Pro	Glu	Tyr	Leu	His	
Asn	Met	Met	Leu	Gly	Ala	Ser	Ser	His	Ser	Tyr	Pro	Glu	Tyr	Leu	His	
	775						780				785					
tgt	ttt	gat	acc	tat	gct	cca	tac	atc	aaa	ctg	aat	ctg	acc	tat	ata	2515
Cys	Phe	Asp	Thr	Tyr	Ala	Pro	Tyr	Ile	Lys	Leu	Asn	Leu	Thr	Tyr	Ile	
Cys	Phe	Asp	Thr	Tyr	Ala	Pro	Tyr	Ile	Lys	Leu	Asn	Leu	Thr	Tyr	Ile	
	790					795				800					805	
cgt	cag	gac	agc	ttc	tcg	gag	aaa	ggg	aca	gaa	gga	aga	tct	ttt	gat	2563
Arg	Gln	Asp	Ser	Phe	Ser	Glu	Lys	Gly	Thr	Glu	Gly	Arg	Ser	Phe	Asp	
Arg	Gln	Asp	Ser	Phe	Ser	Glu	Lys	Gly	Thr	Glu	Gly	Arg	Ser	Phe	Asp	
				810					815						820	
gac	agc	aac	ctc	ttc	aat	tta	tct	ttg	cct	ata	ggg	gtg	aag	ttt	gag	2611
Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile	Gly	Val	Lys	Phe	Glu	
Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile	Gly	Val	Lys	Phe	Glu	
			825					830						835		
aag	ttc	tct	gat	tgt	aat	gac	ttt	tct	tat	gat	ctg	act	tta	tcc	tat	2659
Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp	Leu	Thr	Leu	Ser	Tyr	
Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp	Leu	Thr	Leu	Ser	Tyr	
			840					845						850		
gtt	cct	gat	ctt	atc	cgc	aat	gat	ccc	aaa	tgc	act	aca	gca	ctt	gta	2707
Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys	Thr	Thr	Ala	Leu	Val	
Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys	Thr	Thr	Ala	Leu	Val	
	855						860				865					



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Fig. 3F (cont.)

```
atc agc gga gcc tct tgg gaa act tat gcc aat aac tta gca cga cag 2755
Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln
Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln
870                               875                               880                               885

gcc ttg caa gtg cgt gca ggc agt cac tac gcc ttc tct cct atg ttt 2803
Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala Phe Ser Pro Met Phe
Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala Phe Ser Pro Met Phe
890                               895                               900

gaa gtg ctc ggc cag ttt gtc ttt gaa gtt cgt gga tcc tca cgg att 2851
Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg Gly Ser Ser Arg Ile
Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg Gly Ser Ser Arg Ile
905                               910                               915

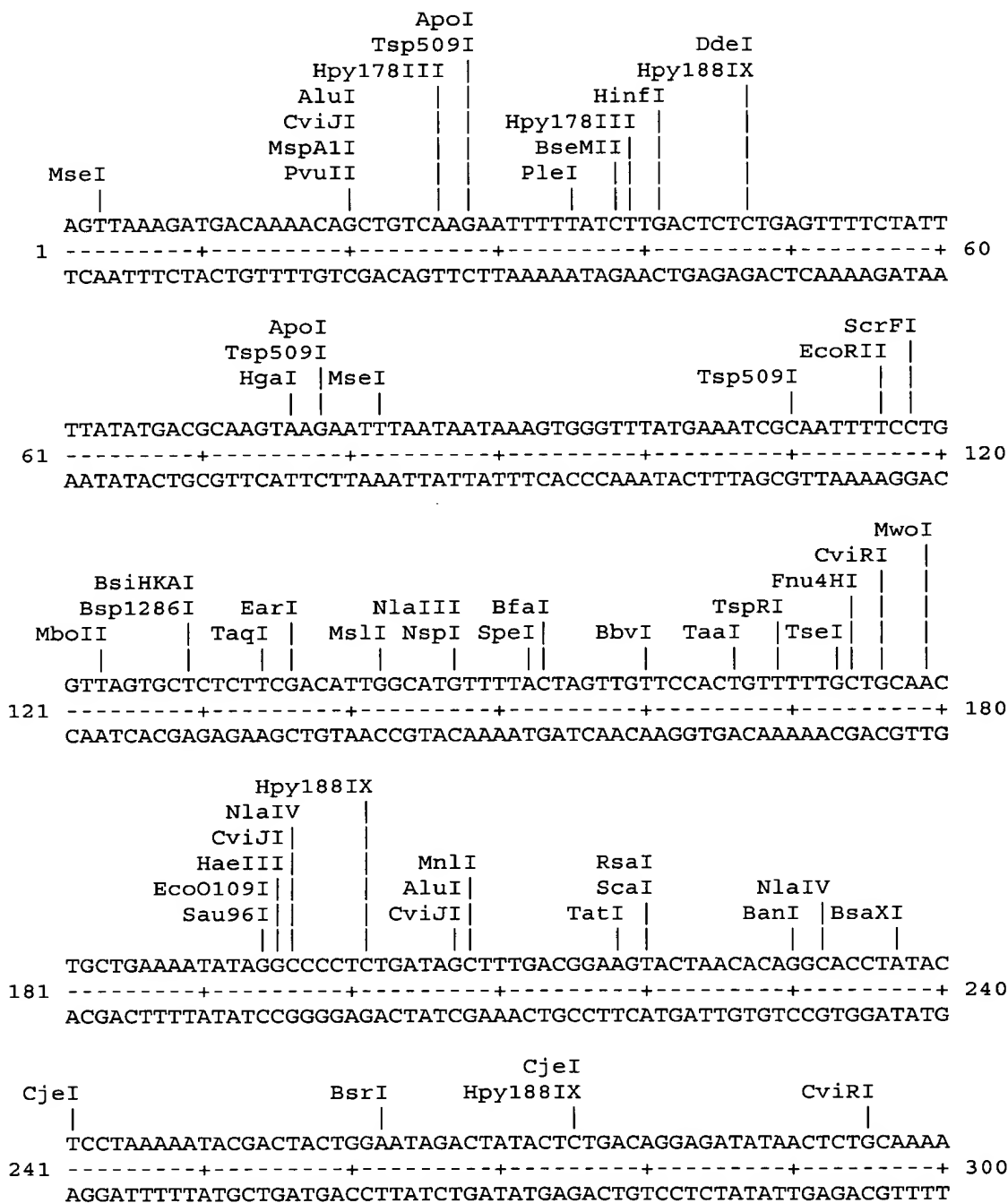
tat aat gta gat ctt ggg ggt aag ttc caa ttc taggagcgtc tctcatgtct 2904
Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe
Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe
920                               925

cagaaattct gagagagatc gcatttagga ttttcttaaa cacgac 2950
```



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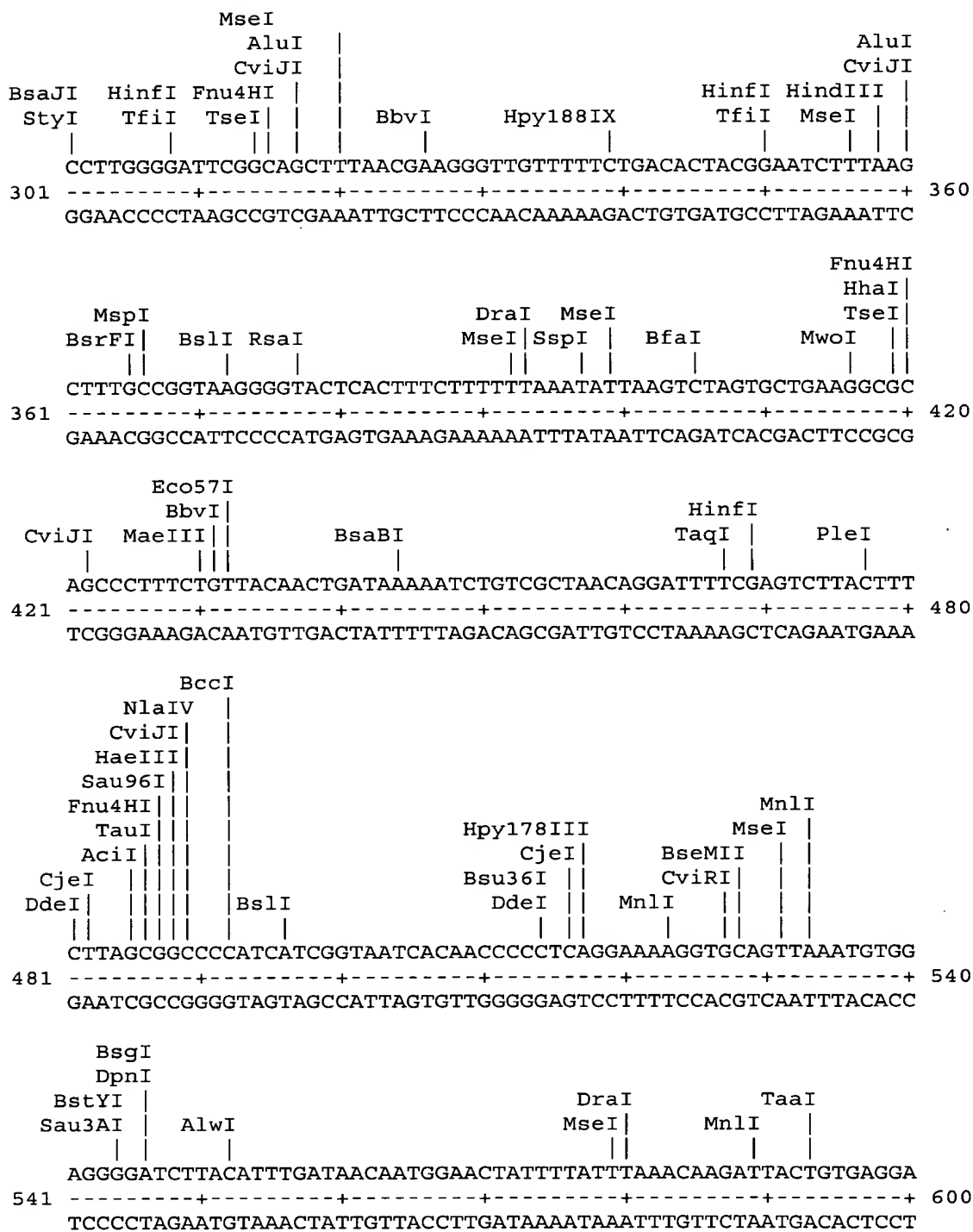
Figure 4 A: Restriction enzyme analysis of CPN100635





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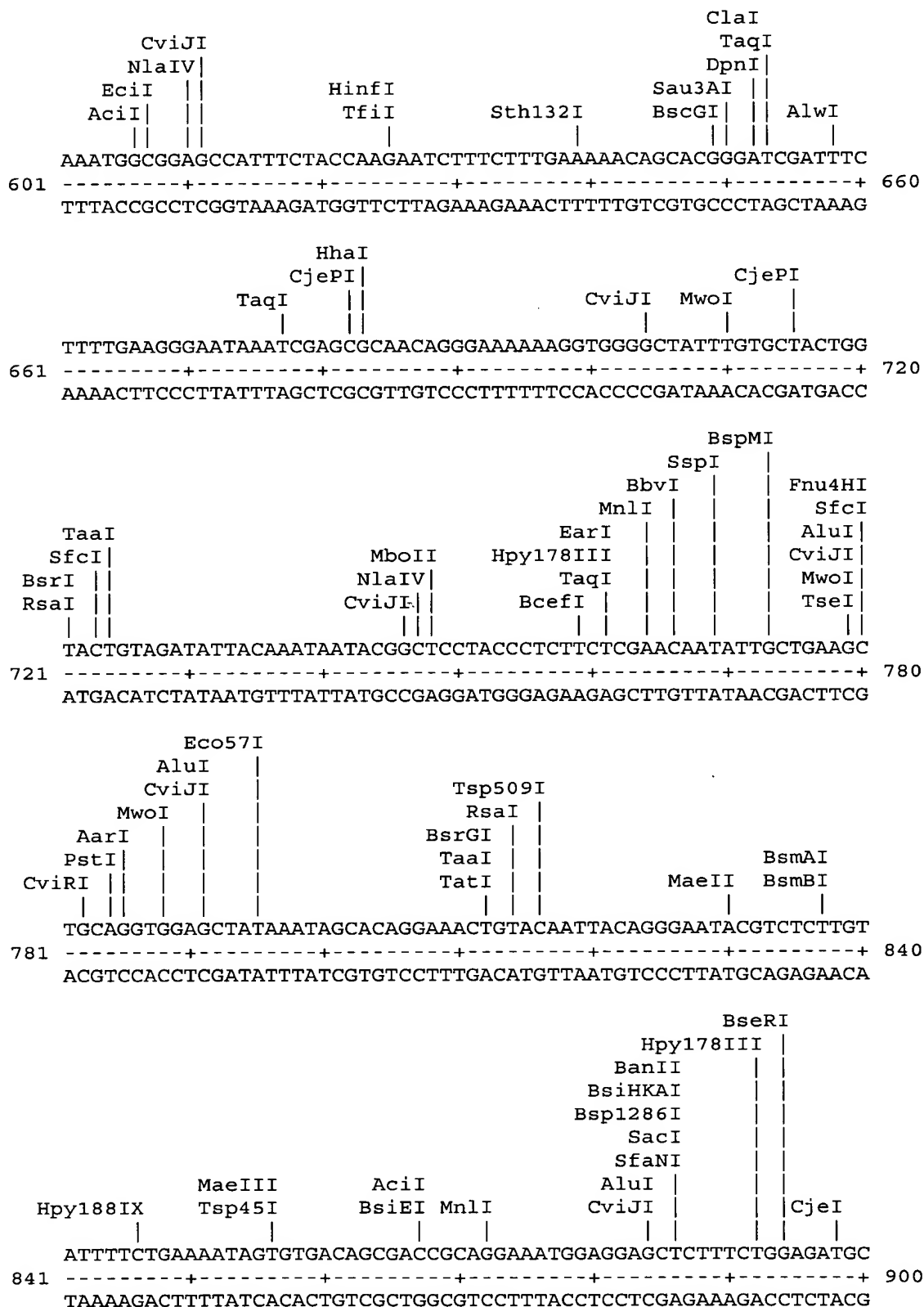
Fig. 4B (cont)





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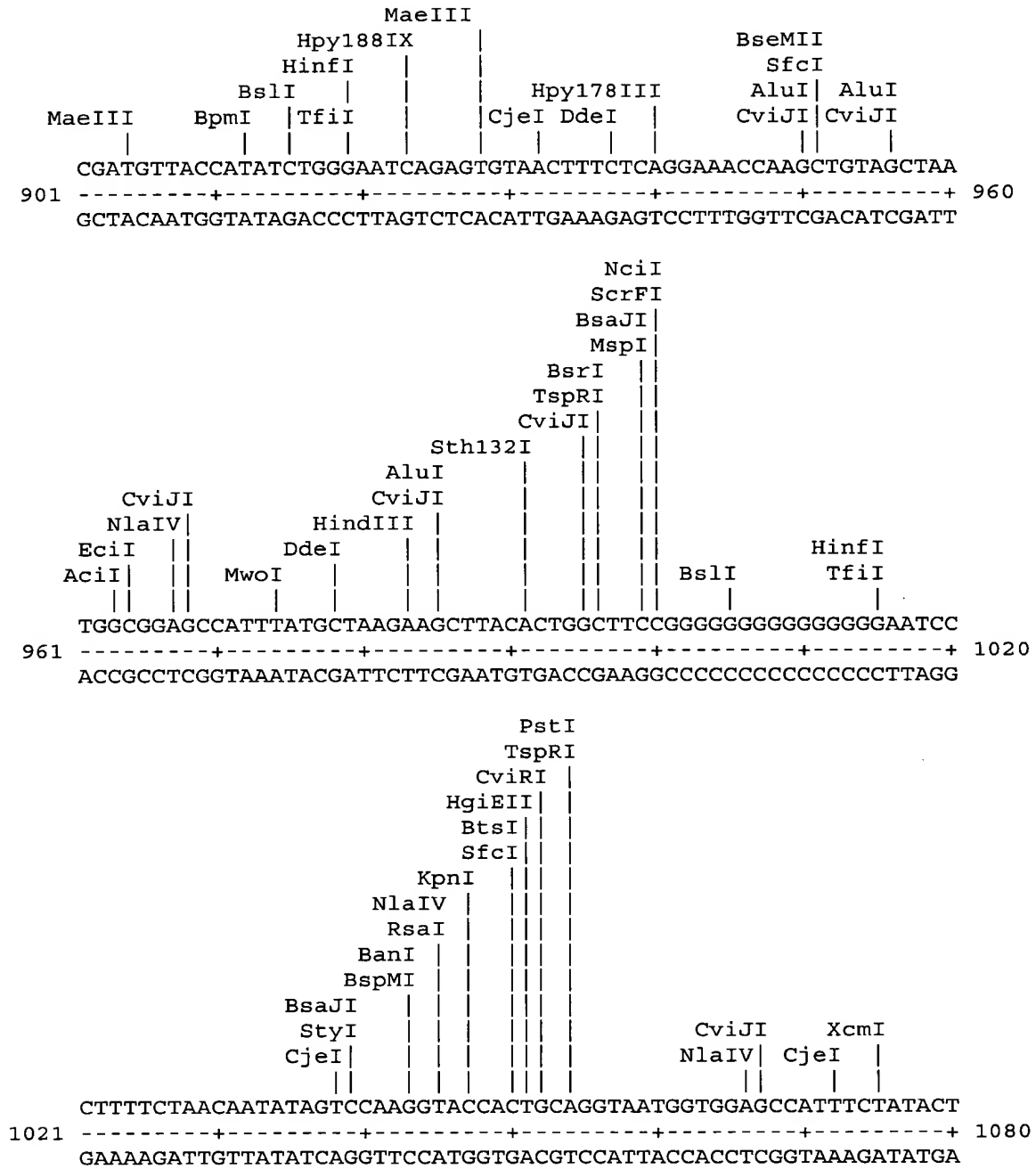
Fig. 4 C (cont.)





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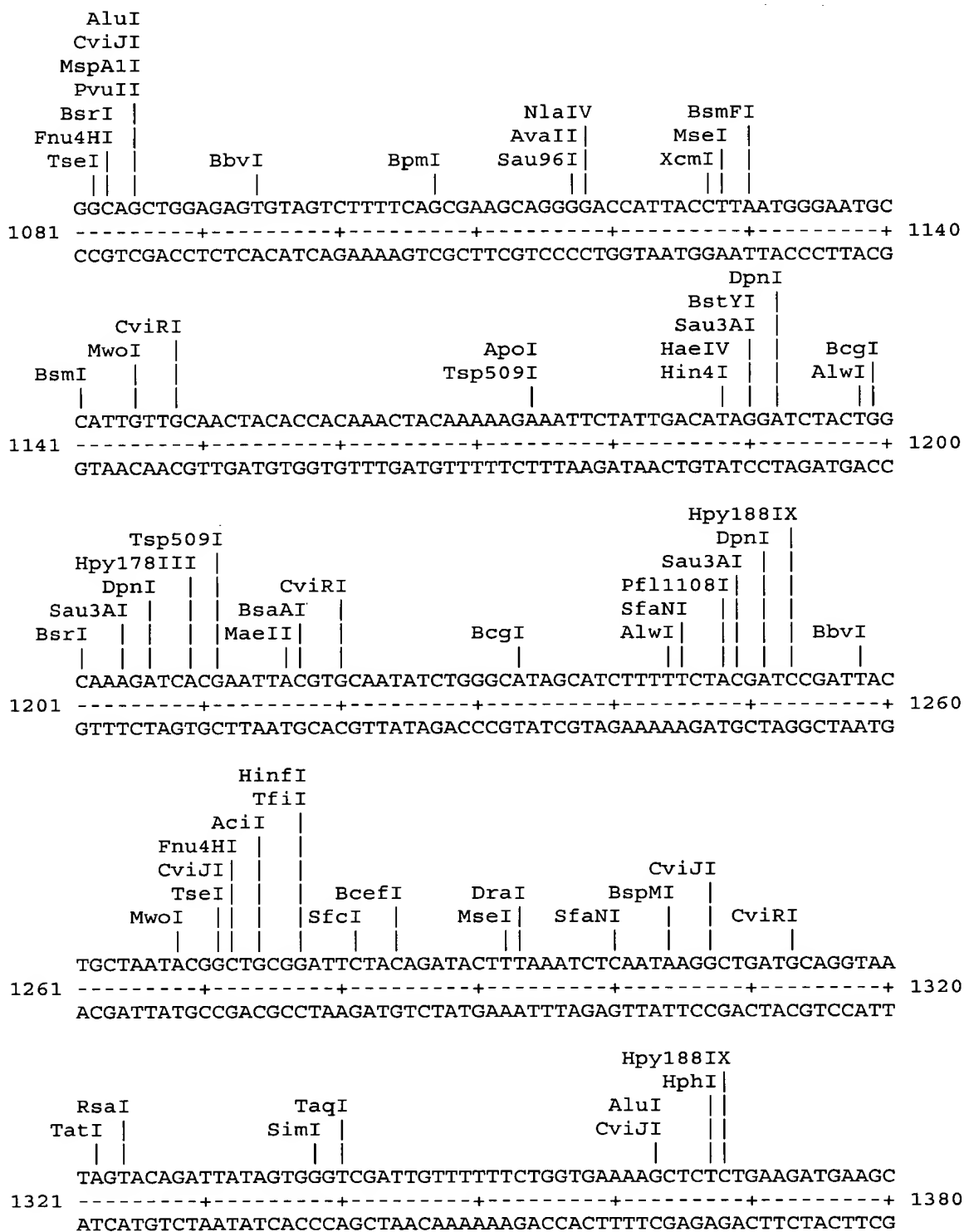
Fig. 4 D (con't)





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Fig. 4 E (cont.)

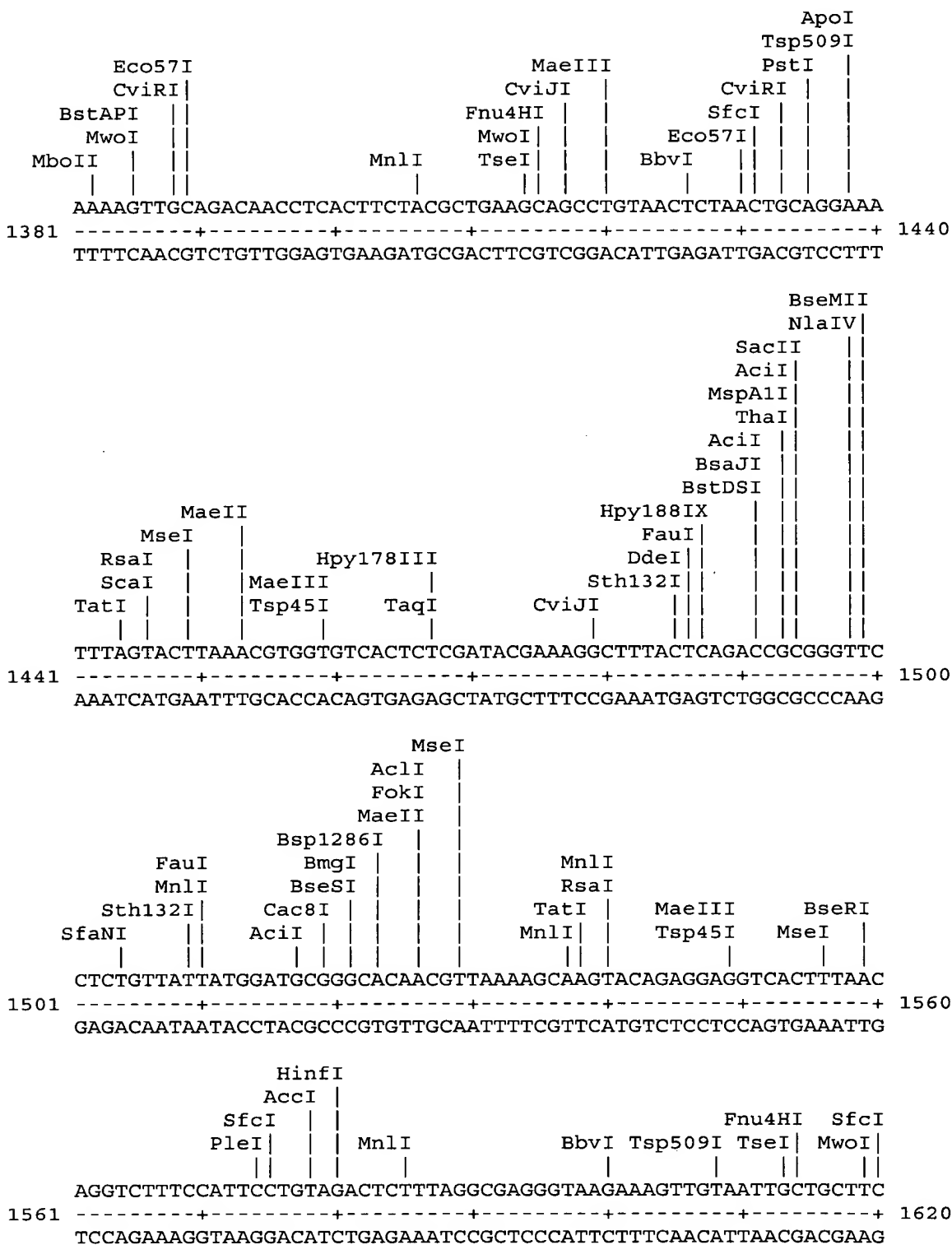






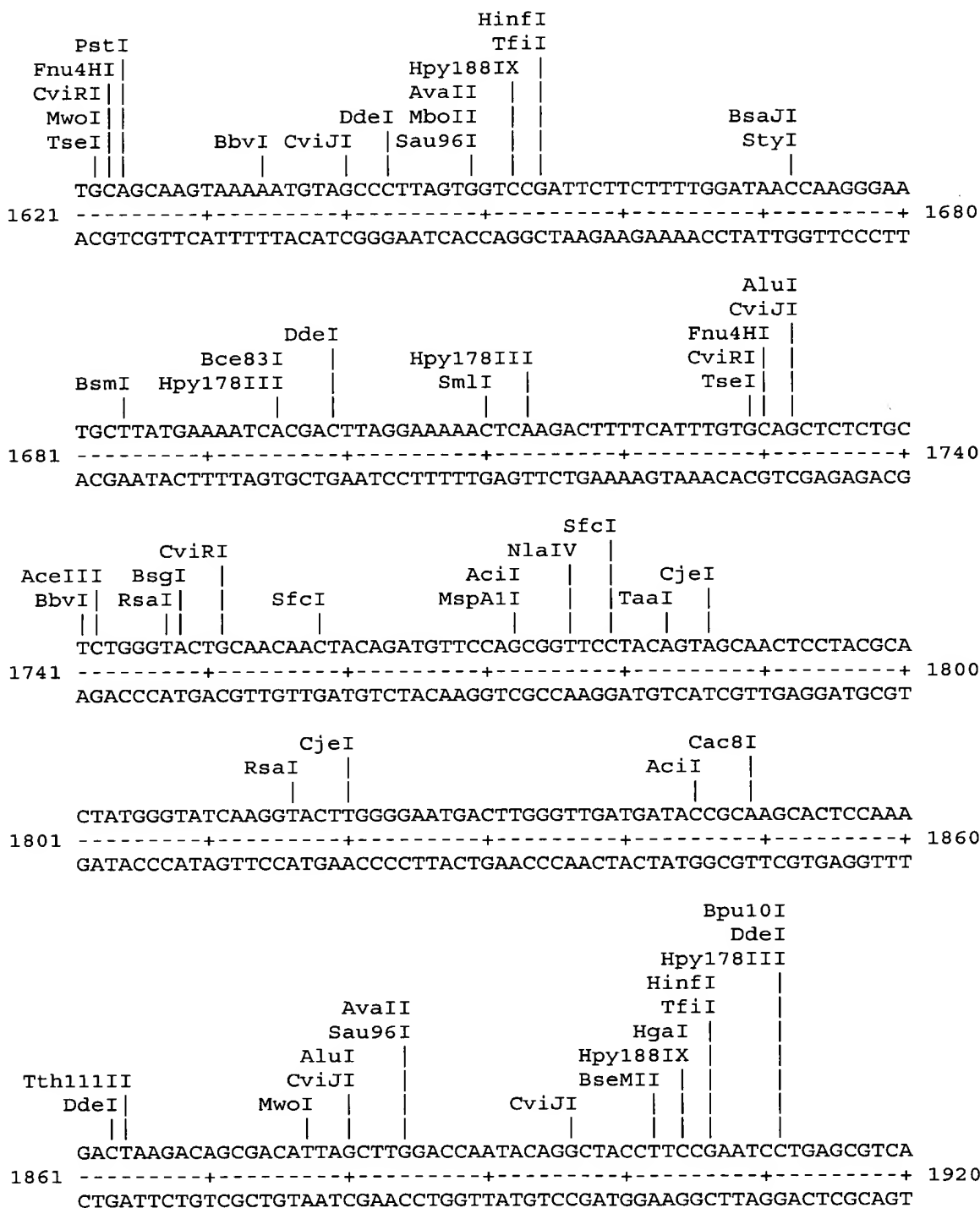
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Fig. 4 F (cont.)



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Fig. 4 G (cont.)



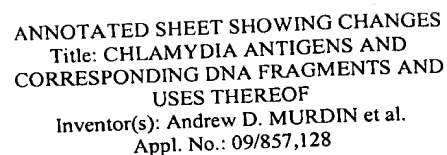


Fig. 4 ~~11~~ (con't)

AvaII  
 EcoO109I  
 Psp5II  
 Sau96I  
 Sse8647I  
 A10I  
 CviJI  
 BstYI  
 FokI  
 Sau3AI  
 DpnI  
 Hpy188IX  
 AlwI  
 HinfI  
 TfiI  
 MwoI  
 HinfI  
 BbvI  
 TaqI  
 DpnI  
 Sau3AI  
 Hpy188IX  
 MnlI  
 PleI  
 HinfI  
 Sth132I  
 CviJI  
 TseI  
 Fnu4HI  
 CviJI  
 TaaI  
 DdeI  
 HaeIV  
 Hln4I  
 Hpy188IX  
 MnlI  
 Fnu4HI  
 CviRI  
 TseI  
 HhaI  
 BbvI  
 Hpy188IX  
 BsgI  
 MseI  
 CviJI  
 AluI  
 BstXI  
 DdeI  
 CviJI  
 NlaIV  
 CviRI  
 BsbI  
 MmeI  
 BsmAI  
 DdeI

AGGACCTTTAGTTCCTAATAGCCTTTGGGGATCTTTTTCAGACATCCAAGCGATTCAAGG  
 TCCTGGAAATCAAGGATTATCGGAAACCCCTAGAAAAAGTCTGTAGGTTTCGCTAAGTTCC  
 TGTCATAGAGAGAAGTGCTTTGACTCTTTGTTCAGATCGAGGCTTCTGGGCTGCGGGAGT  
 ACAGTATCTCTCTTCACGAAACTGAGAAACAAGTCTAGCTCCGAAGACCCGACGCCCTCA  
 CGCCAATTTCTTAGATAAAAGATAAGAAAGGGGAAAAACGCAAATACCGTCATAAATCTGG  
 GCGGTTAAAGAATCTATTTCTATTCTTTCCCTTTTTGCGTTTATGGCAGTATTTAGACC  
 TGGATATGCTATCGGAGGTGCAGCGCAAACCTTGTTCTGAAAACCTTAATTAGCTTTGCCTT  
 ACCTATACGATAGCCTCCACGTCGCGTTTGAACAAGACTTTTGAATTAATCGAAACGGAA  
 TTGCCAACTCTTTGGTAGCGATAAAGATTTCTTAGTCGCTAAAAATCATACTGATACCTA  
 AACGGTTGAGAAACCATCGCTATTTCTAAAGAATCAGCGATTTTGTAGTATGACTATGGAT  
 TGCAGGAGCCTTCTATATCCAACACATTACAGAATGTAGTGGGTTTCATAGGTTGTCTCTT  
 ACGTCCTCGGAAGATATAGGTTGTGTAATGTCTTACATCACCCAAGTATCCAACAGAGAA

1921  
 1981  
 2041  
 2101  
 2161  
 2221

1980  
 2040  
 2100  
 2160  
 2220  
 2280



Fig. 41 (cont.)

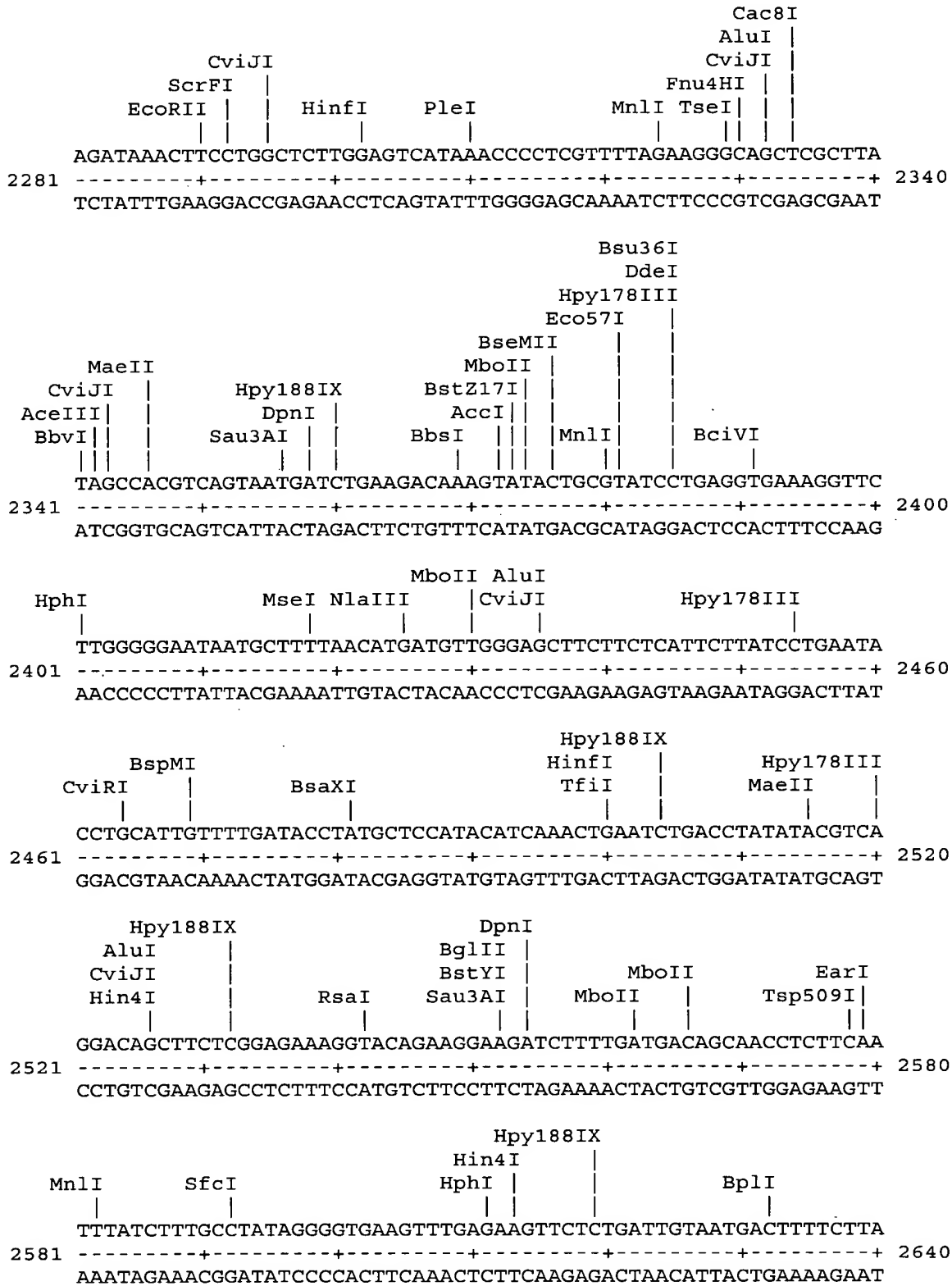
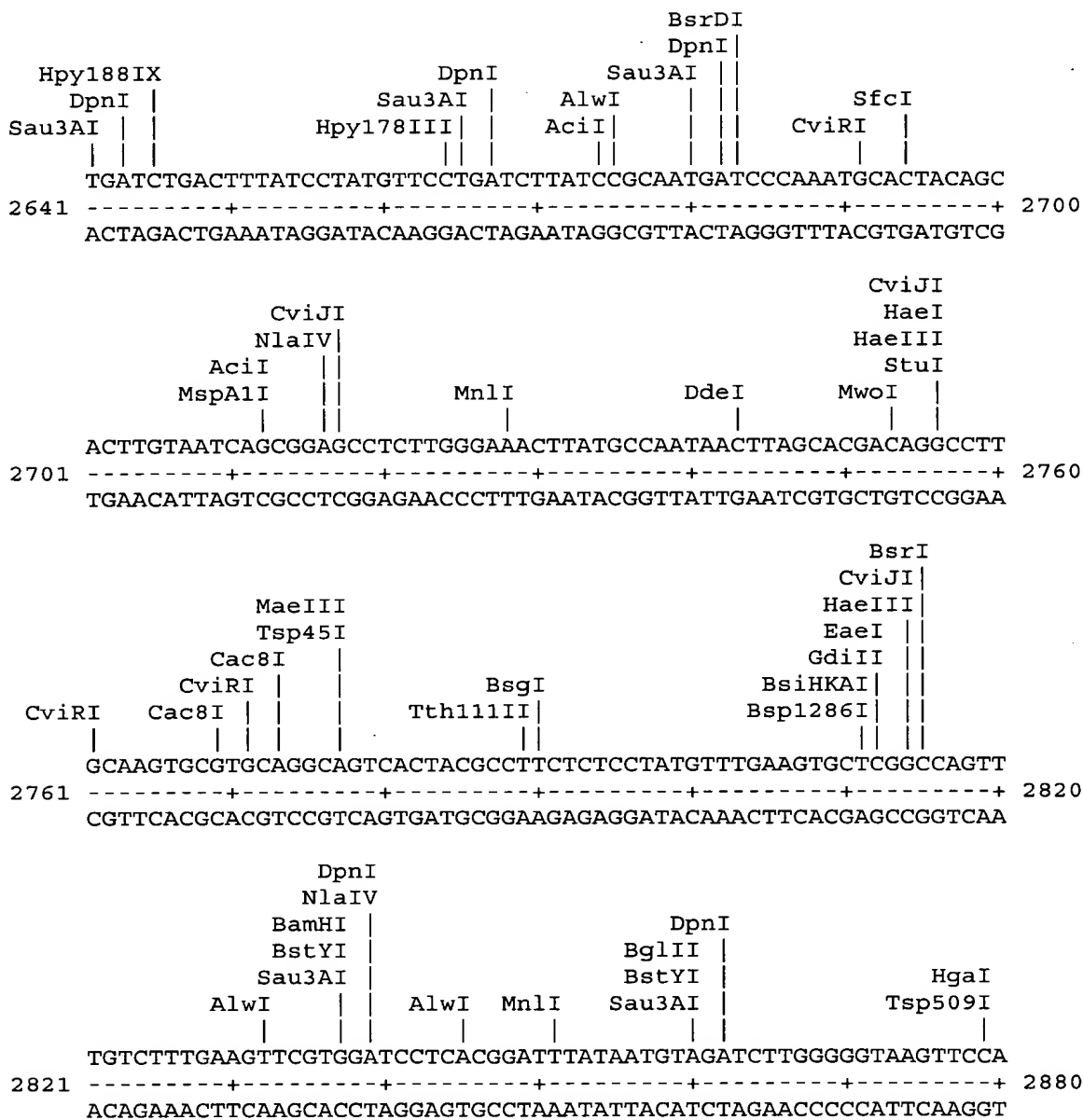


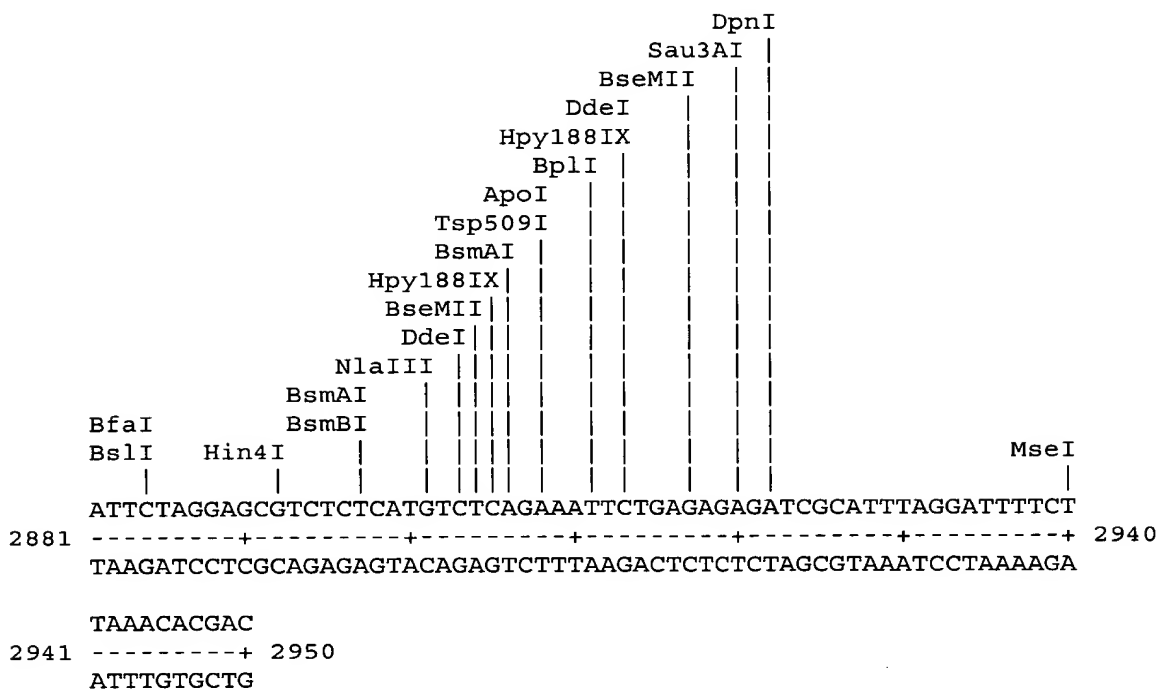
Fig. 4 (cont.)





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Fig. 4 K (cont)





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ANNOTATED SHEET SHOWING CHANGES  
Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128

Figure 5 A: Nucleotide and deduced amino acid sequence of CPN100638

```
tgtagattct taacttacta gtctctcctt tcctcttgc ttcctttaatt tattgcagta 60
tgtgggtgaaa taatttggtta aaccacctat agccctctac atg aaa tcc tct ctt 115
Met Lys Ser Ser Leu
1 5
cat tgg ttt tta atc tcg tca tct tta gca ctt ccc ttg tca cta aat 163
His Trp Phe Leu Ile Ser Ser Ser Leu Ala Leu Pro Leu Ser Leu Asn
10 15 20
ttc tct gcg ttt gct gct gtt gtt gaa atc aat cta gga cct acc aat 211
Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn Leu Gly Pro Thr Asn
25 30 35
agc ttc tct gga cca gga acc tac act cct cca gcc caa aca aca aat 259
Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro Ala Gln Thr Thr Asn
40 45 50
gca gat gga act atc tat aat cta aca ggg gat gtc tca atc acc aat 307
Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp Val Ser Ile Thr Asn
55 60 65
gca gga tct ccg aca gct cta acc gct tcc tgc ttt aaa gaa act act 355
Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys Phe Lys Glu Thr Thr
70 75 80 85
ggg aat ctt tct ttc caa ggc cac ggc tac caa ttt ctc cta caa aat 403
Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln Phe Leu Leu Gln Asn
90 95 100
atc gat gcg gga gcg aac tgt acc ttt acc aat aca gct gca aat aag 451
Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn Thr Ala Ala Asn Lys
105 110 115
ctt ctc tcc ttt tca gga ttc tcc tat ttg tca cta ata caa acc acg 499
Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser Leu Ile Gln Thr Thr
120 125 130
aat gct acc aca gga aca gga gcc atc aag tcc aca gga gct tgt tct 547
Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser Thr Gly Ala Cys Ser
135 140 145
att cag tcg aac tat agt tgc tac ttt ggc caa aac ttt tct aat gac 595
Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln Asn Phe Ser Asn Asp
150 155 160 165
aat gga ggc gcc ctc caa ggc agc tct atc agt cta tcg cta aac ccc 643
Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser Leu Ser Leu Asn Pro
170 175 180
aac cta acg ttt gcc aaa aac aaa gca acg caa aaa ggg ggt gcc ctc 691
Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln Lys Gly Gly Ala Leu
185 190 195
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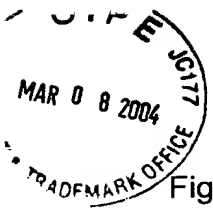


Fig. 5B (cont)

tat tcc acg gga ggg att aca att aac aat acg tta aac tca gca tca	739
Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr Leu Asn Ser Ala Ser	
200 205 210	
ttt tct gaa aat acc gcg gcg aac aat ggc gga gcc att tac acg gaa	787
Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly Ala Ile Tyr Thr Glu	
215 220 225	
gct agc agt ttt att agc agc aac aaa gca att agc ttt ata aac aat	835
Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile Ser Phe Ile Asn Asn	
230 235 240 245	
agt gtg acc gca acc tca gct aca ggg gga gcc att tac tgt agt agt	883
Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala Ile Tyr Cys Ser Ser	
250 255 260	
aca tca gcc ccc aaa cca gtc tta act cta tca gac aac ggg gaa ctg	931
Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser Asp Asn Gly Glu Leu	
265 270 275	
aac ttt ata gga aat aca gca att act agt ggt ggg gcg att tat act	979
Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly Gly Ala Ile Tyr Thr	
280 285 290	
gac aat cta gtt ctt tct tct gga gga cct acg ctt ttt aaa aac aac	1027
Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr Leu Phe Lys Asn Asn	
295 300 305	
tct ggc tat gat act gca gct ccc tta gga gga gca att gcg att gct	1075
Ser Gly Tyr Asp Thr Ala Ala Pro Leu Gly Gly Ala Ile Ala Ile Ala	
310 315 320 325	
gac tct gga tct ttg agt ctt tcg gct ctt ggt gga gac atc act ttt	1123
Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly Gly Asp Ile Thr Phe	
330 335 340	
gaa gga aac aca gta gtc aaa gga gct tct tcg agt cag acc act acc	1171
Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser Ser Gln Thr Thr Thr	
345 350 355	
aga aat tct att aac atc gga aac acc aat gct aag att gta cag ctg	1219
Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala Lys Ile Val Gln Leu	
360 365 370	
cga gcc tct caa ggc aat act atc tac ttc tat gat cct ata aca act	1267
Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr Asp Pro Ile Thr Thr	
375 380 385	
agc atc act gca gct ctc tca gat gct cta aac tta aat ggt cct gac	1315
Ser Ile Thr Ala Ala Leu Ser Asp Ala Leu Asn Leu Asn Gly Pro Asp	
390 395 400 405	
ctt gca ggg aat cct gca tat caa gga acc atc gta ttt tct gga gag	1363
Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile Val Phe Ser Gly Glu	
410 415 420	



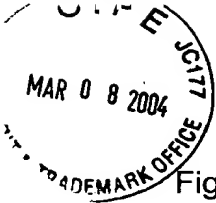


Fig. 5 C (con't)

aag ctc tcg gaa gca gaa gct gca gaa gct gat aat ctc aaa tct aca	1411
Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp Asn Leu Lys Ser Thr	
425 430 435	
att cag caa cct cta act ctt gcg gga ggg caa ctc tct ctt aaa tca	1459
Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln Leu Ser Leu Lys Ser	
440 445 450	
gga gtc act cta gtt gct aag tcc ttt tcg caa tct ccg ggc tct acc	1507
Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln Ser Pro Gly Ser Thr	
455 460 465	
ctc ctc atg gat gca ggg acc aca tta gaa acc gct gat ggg atc act	1555
Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr Ala Asp Gly Ile Thr	
470 475 480 485	
atc aat aat ctt gtt ctc aat gta gat tcc tta aaa gag acc aag aag	1603
Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu Lys Glu Thr Lys Lys	
490 495 500	
ggc acg cta aaa gca aca caa gca agt cag aca gtc act tta tct gga	1651
Gly Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr Val Thr Leu Ser Gly	
505 510 515	
tcg ctc tct ctt gta gat cct tct gga aat gtc tac gaa gat gtc tct	1699
Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val Tyr Glu Asp Val Ser	
520 525 530	
tgg aat aac cct caa gtc ttt tct tgt ctc act ctt act gct gac gac	1747
Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr Leu Thr Ala Asp Asp	
535 540 545	
ccc gcg aat att cac atc aca gac tta gct gct gat ccc cta gaa aaa	1795
Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala Asp Pro Leu Glu Lys	
550 555 560 565	
aat cct atc cat tgg gga tac caa ggg aat tgg gca tta tct tgg caa	1843
Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp Ala Leu Ser Trp Gln	
570 575 580	
gag gat act gcg act aaa tcc aaa gca gcg act ctt acc tgg aca aaa	1891
Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr Leu Thr Trp Thr Lys	
585 590 595	
aca gga tac aat ccg aat cct gag cgt cgt gga acc tta gtt gct aac	1939
Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly Thr Leu Val Ala Asn	
600 605 610	
acg cta tgg gga tcc ttt gtt gat gtg cgc tcc ata caa cag ctt gta	1987
Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile Gln Gln Leu Val	
615 620 625	
gcc act aaa gta cgc caa tct caa gaa act cgc ggc atc tgg tgt gaa	2035
Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg Gly Ile Trp Cys Glu	
630 635 640 645	

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Fig. 5D (con't)

ggg atc tcg aac ttc ttc cat aaa gat agc acg aag ata aat aaa ggt	2083
Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr Lys Ile Asn Lys Gly	
650 655 660	
ttt cgc cac ata agt gca ggt tat gtt gta gga gcg act aca aca tta	2131
Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly Ala Thr Thr Thr Leu	
665 670 675	
gct tct gat aat ctt atc act gca gcc ttc tgc caa tta ttc ggg aaa	2179
Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys Gln Leu Phe Gly Lys	
680 685 690	
gat aga gat cac ttt ata aat aaa aat aga gct tct gcc tat gca gct	2227
Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala Ser Ala Tyr Ala Ala	
695 700 705	
tct ctc cat ctc cag cat cta gcg acc ttg tct tct cca agc ttg tta	2275
Ser Leu His Leu Gln His Leu Ala Thr Leu Ser Ser Pro Ser Leu Leu	
710 715 720 725	
cgc tac ctt cct gga tct gaa agt gag cag cct gtc ctc ttt gat gct	2323
Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro Val Leu Phe Asp Ala	
730 735 740	
cag atc agc tat atc tat agt aaa aat act atg aaa acc tat tac acc	2371
Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met Lys Thr Tyr Tyr Thr	
745 750 755	
caa gca cca aag gga gag agc tcg tgg tat aat gac ggt tgc gct ctg	2419
Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn Asp Gly Cys Ala Leu	
760 765 770	
gaa ctt gcg agc tcc cta cca cac act gct tta agc cat gag ggt ctc	2467
Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu Ser His Glu Gly Leu	
775 780 785	
ttc cac gcg tat ttt cct ttc atc aaa gta gaa gct tcg tac ata cac	2515
Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu Ala Ser Tyr Ile His	
790 795 800 805	
caa gat agc ttc aaa gaa cgt aat act acc ttg gta cga tct ttc gat	2563
Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu Val Arg Ser Phe Asp	
810 815 820	
agc ggt gat tta att aac gtc tct gtg cct att gga att acc ttc gag	2611
Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile Gly Ile Thr Phe Glu	
825 830 835	
aga ttc tcg aga aac gag cgt gcg tct tac gaa gct act gtc atc tac	2659
Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu Ala Thr Val Ile Tyr	
840 845 850	
gtt gcc gat gtc tat cgt aag aat cct gac tgc acg aca gct ctc cta	2707
Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys Thr Thr Ala Leu Leu	
855 860 865	

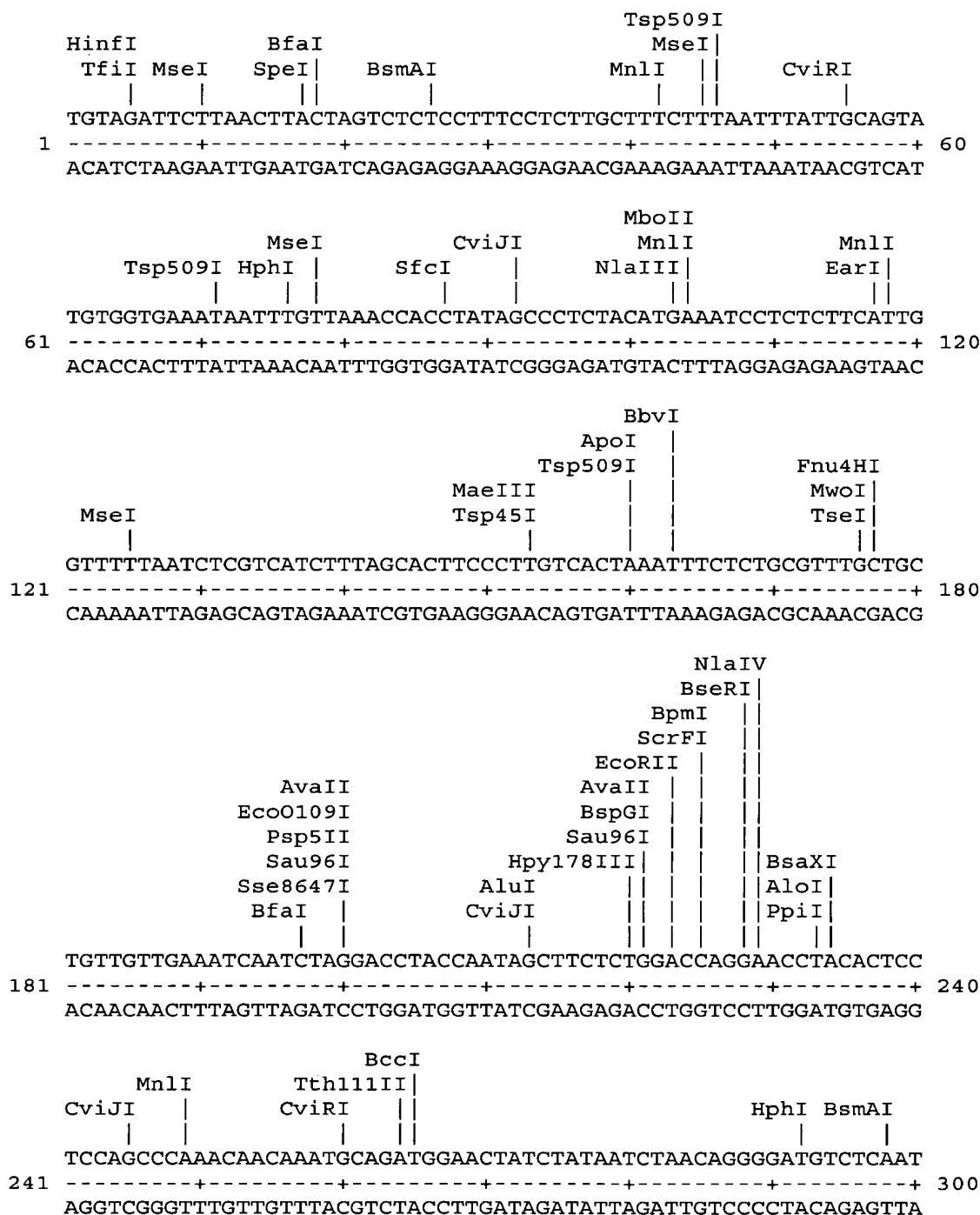


Fig. 5 E (cont.)

atc aac aat acc tcg tgg aaa act aca gga acg aat ctc tca aga caa	2755
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870 875 880 885	
gct ggt atc gga aga gca ggg atc ttt tat gcc ttc tct cca aat ctt	2803
Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala Phe Ser Pro Asn Leu	
890 895 900	
gag gtc aca agt aac cta tct atg gaa att cgt gga tct tca cgc agc	2851
Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg Gly Ser Ser Arg Ser	
905 910 915	
tac aat gca gat ctt gga ggt aag ttc cag ttc taaaagcgtt cctgatccct	2904
Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe	
920 925	
tagaaaattct aagagatcct gagtgtatct agggacttct caaaga	2950



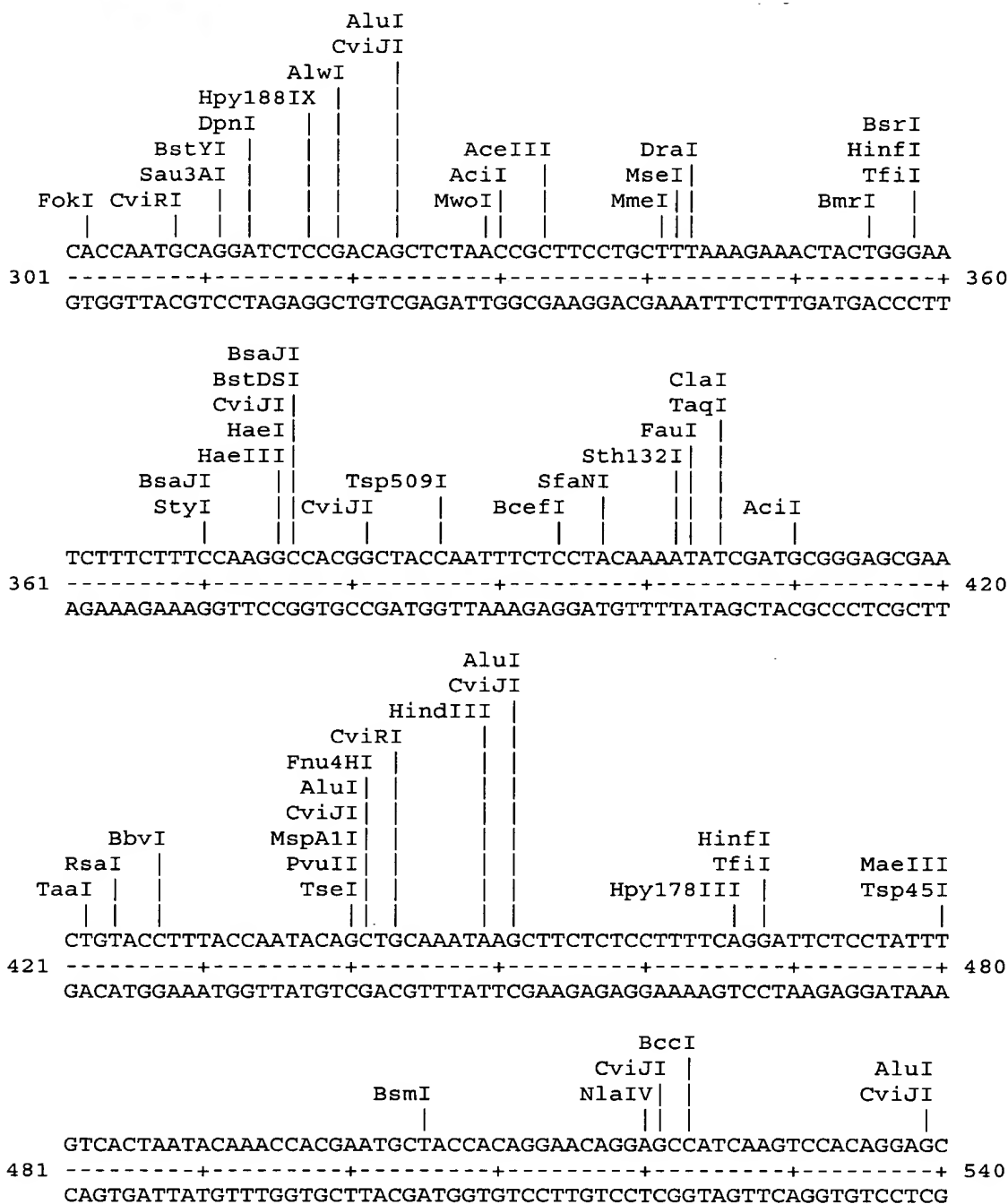
Figure 6 A: Restriction enzyme analysis of CPN100638





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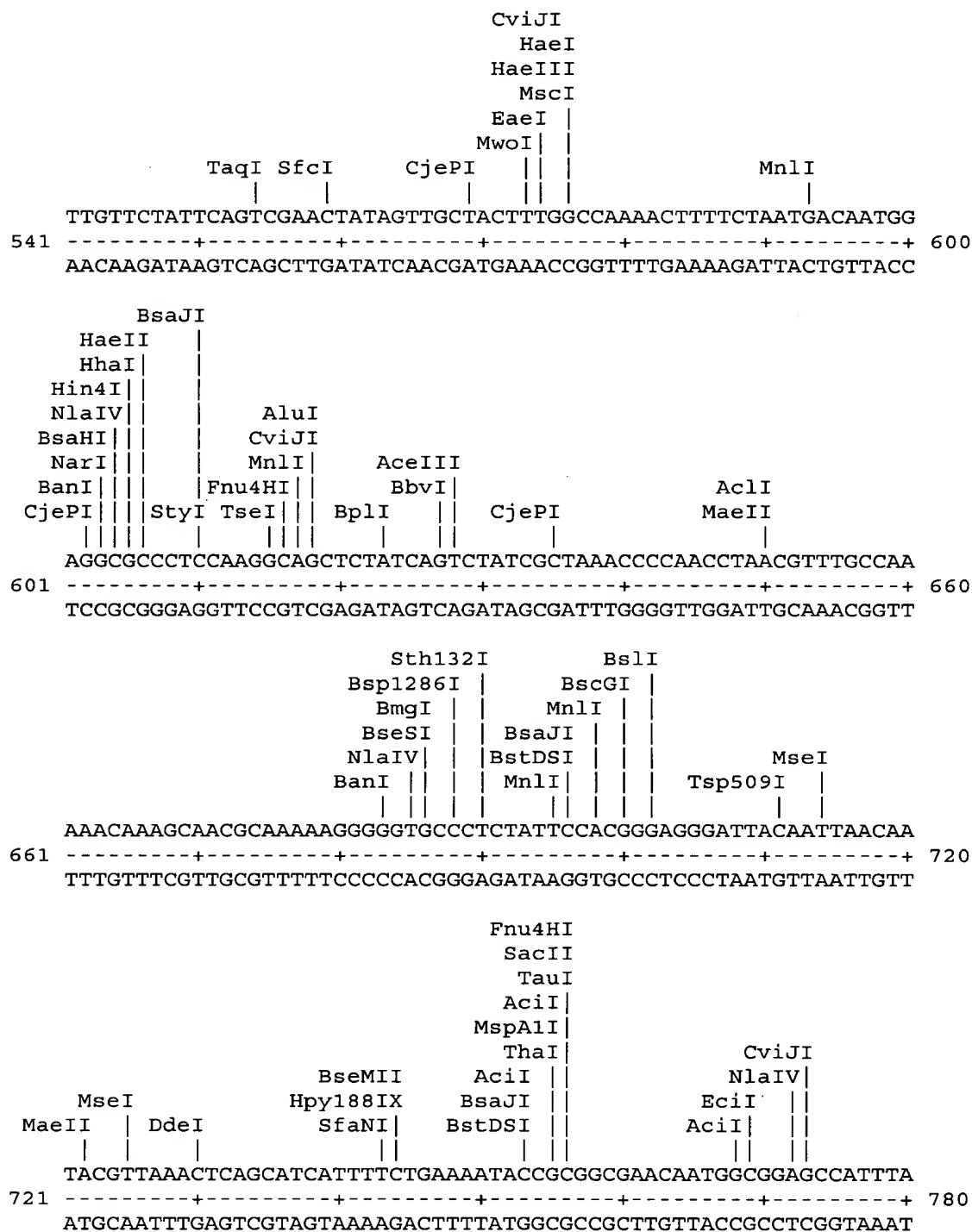
Fig. 6 B (cont)





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Fig. 6 C (cont)

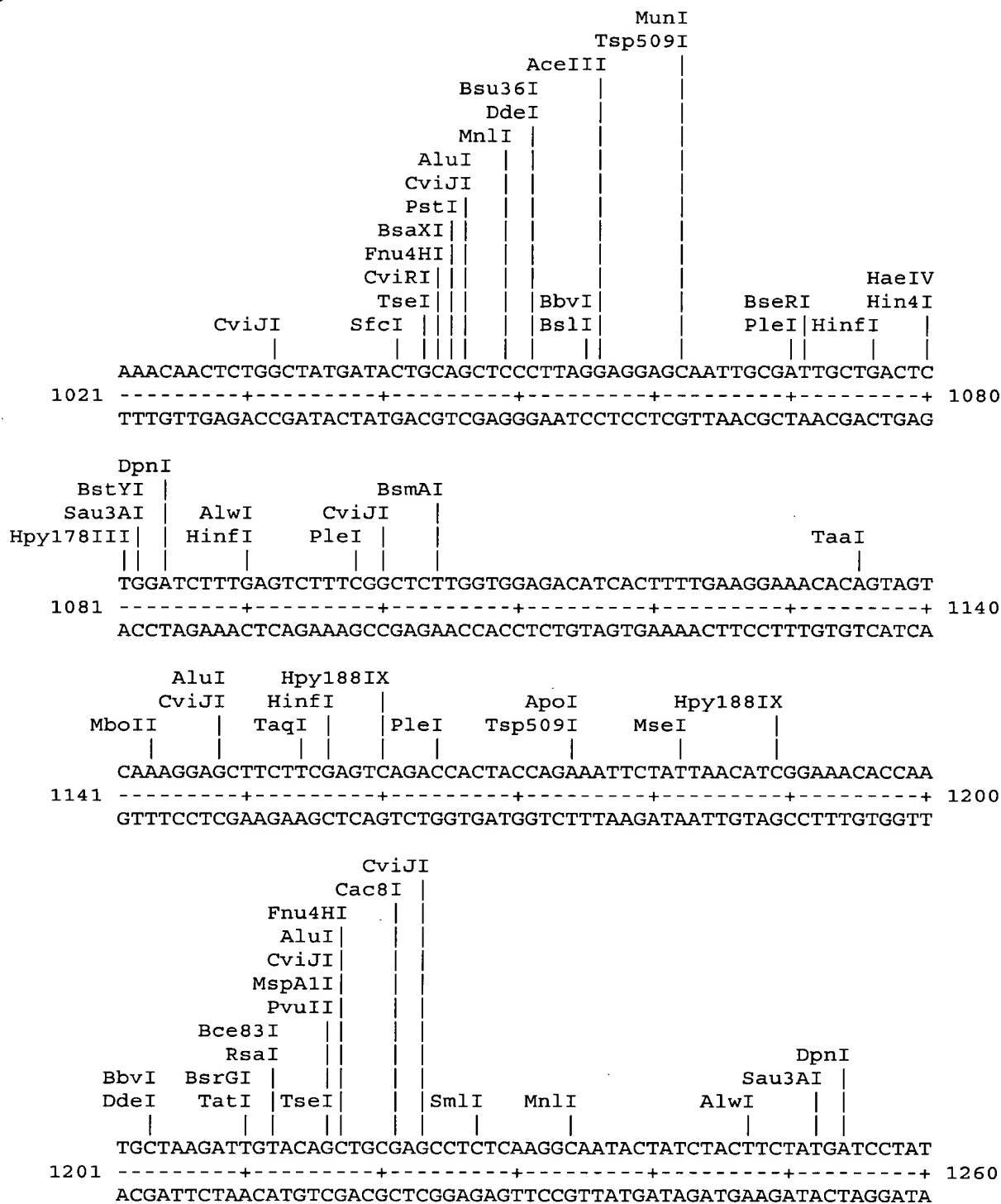


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Fig. 6 E (con't)

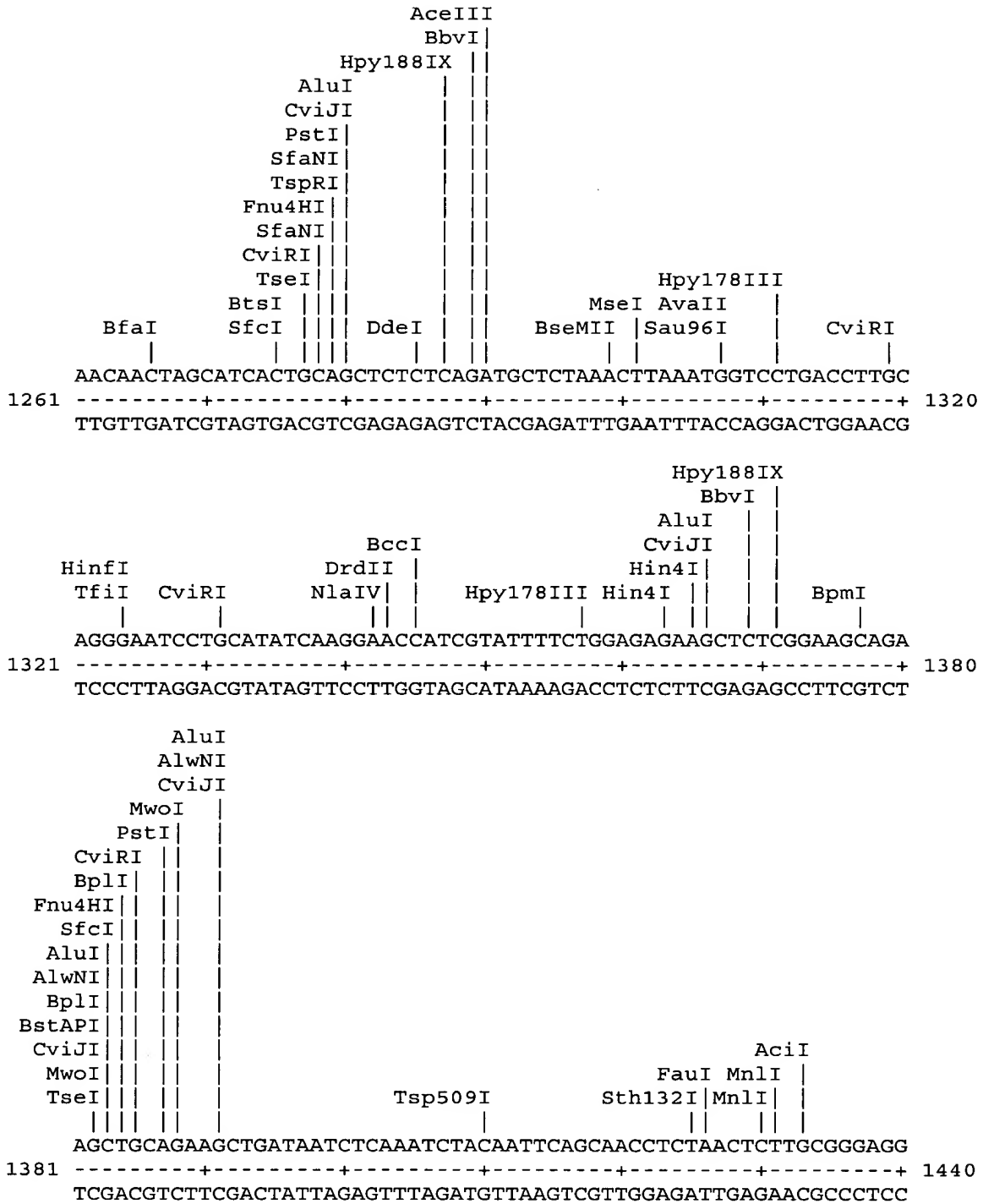






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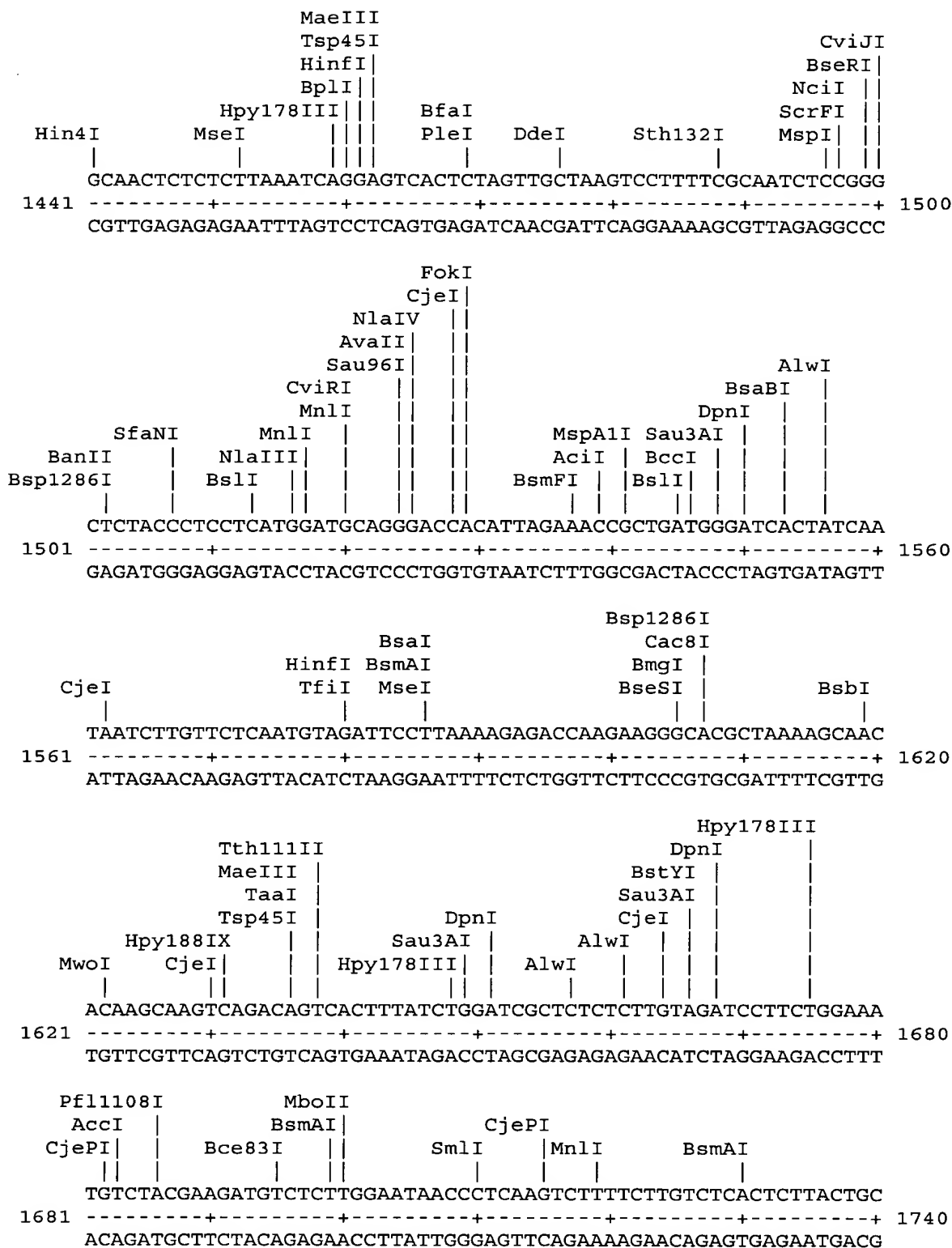
Fig. 6F (cont.)





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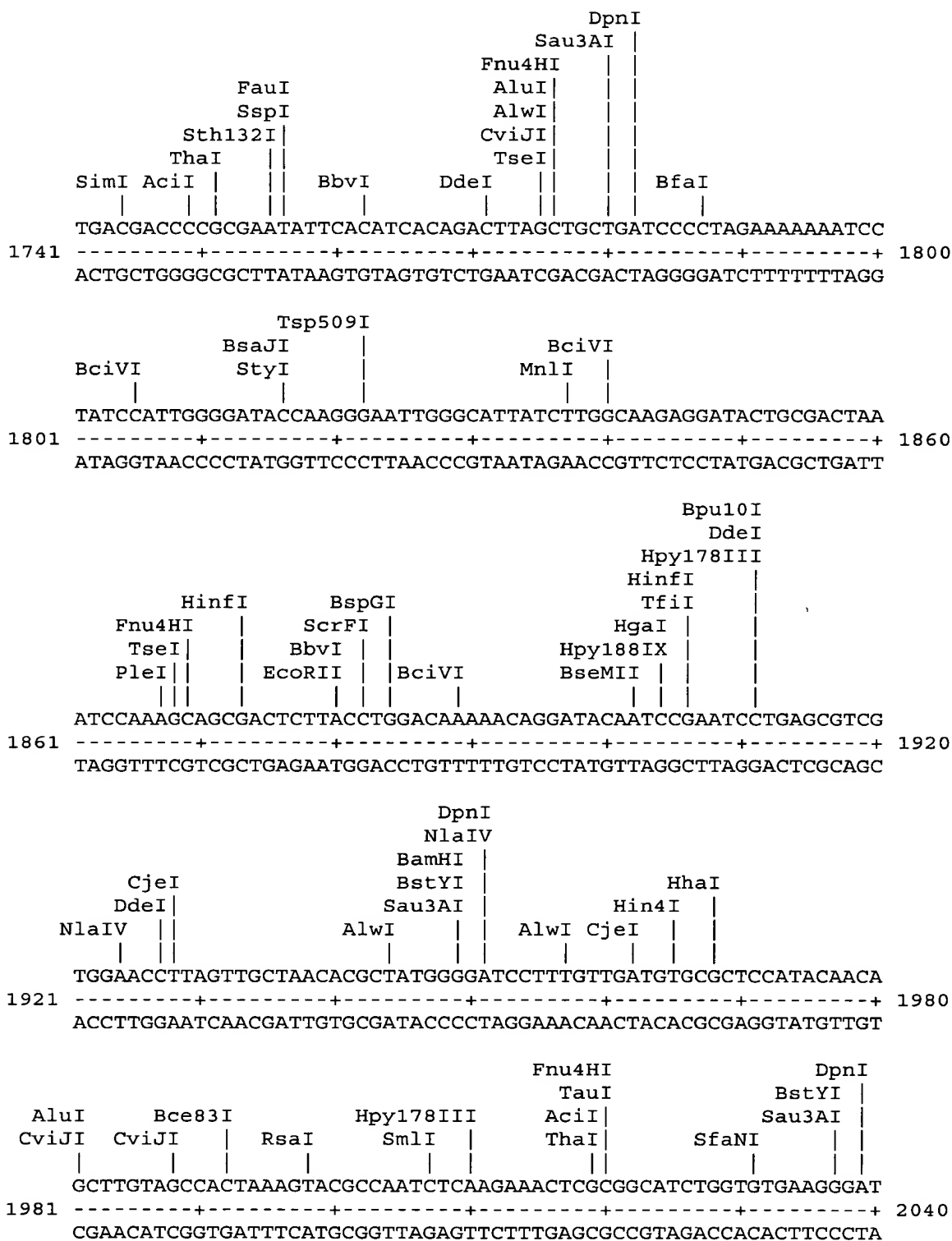
Fig. 6 G (cont)





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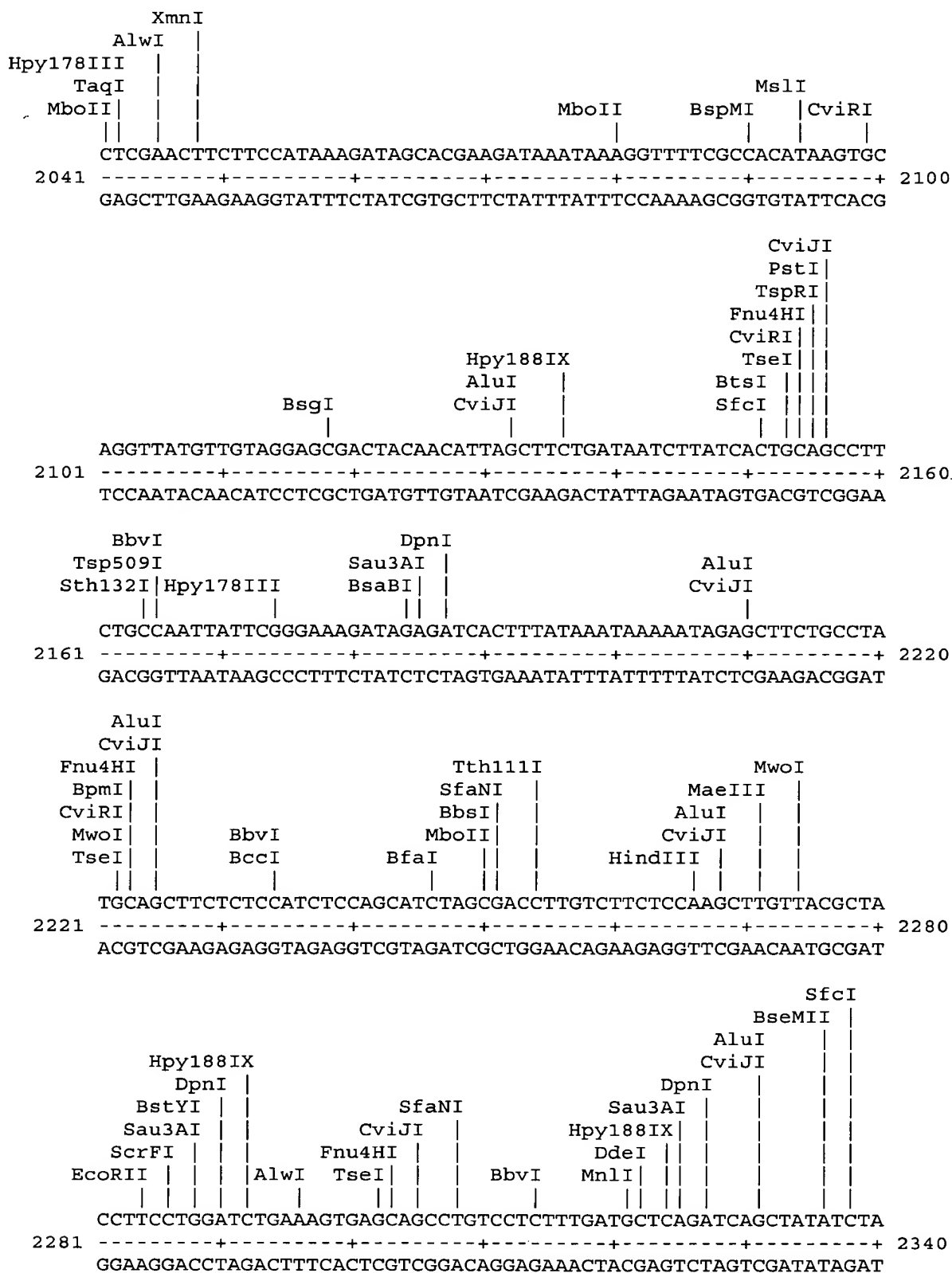
Fig. 6H (cont)





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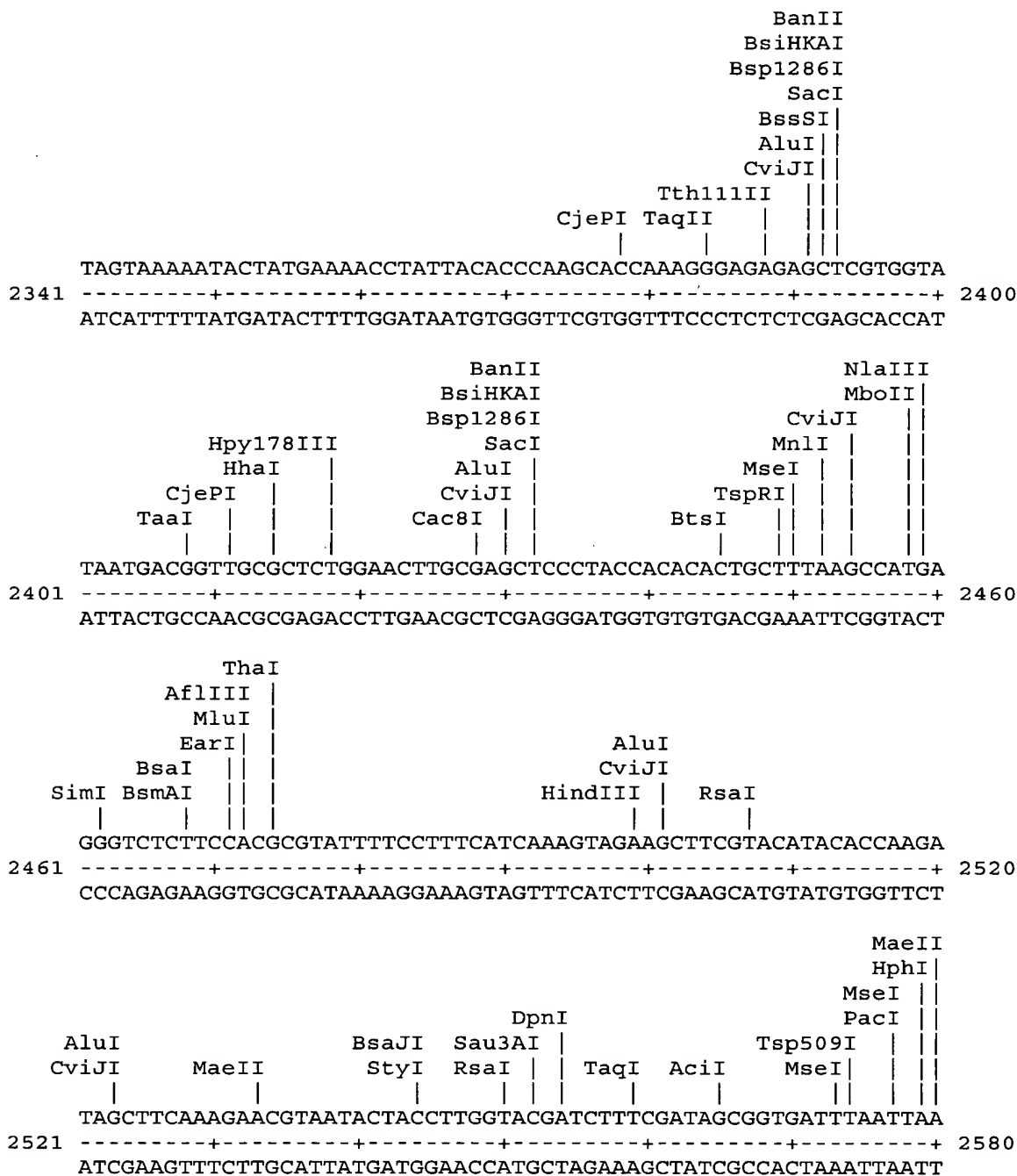
Fig. 6 (cont.)





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Fig. 6-1 (cont)





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Fig. 6 K (cont.)

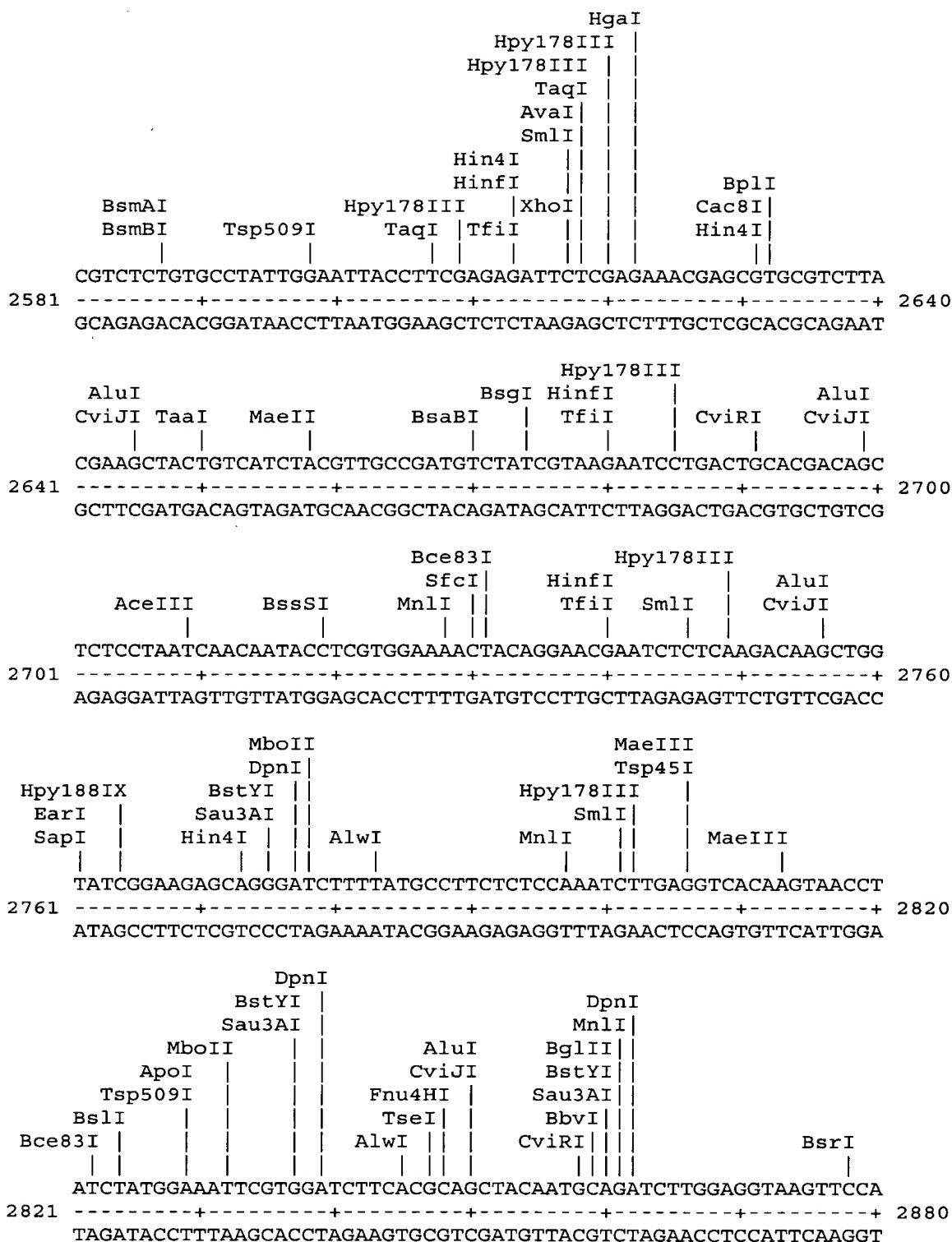
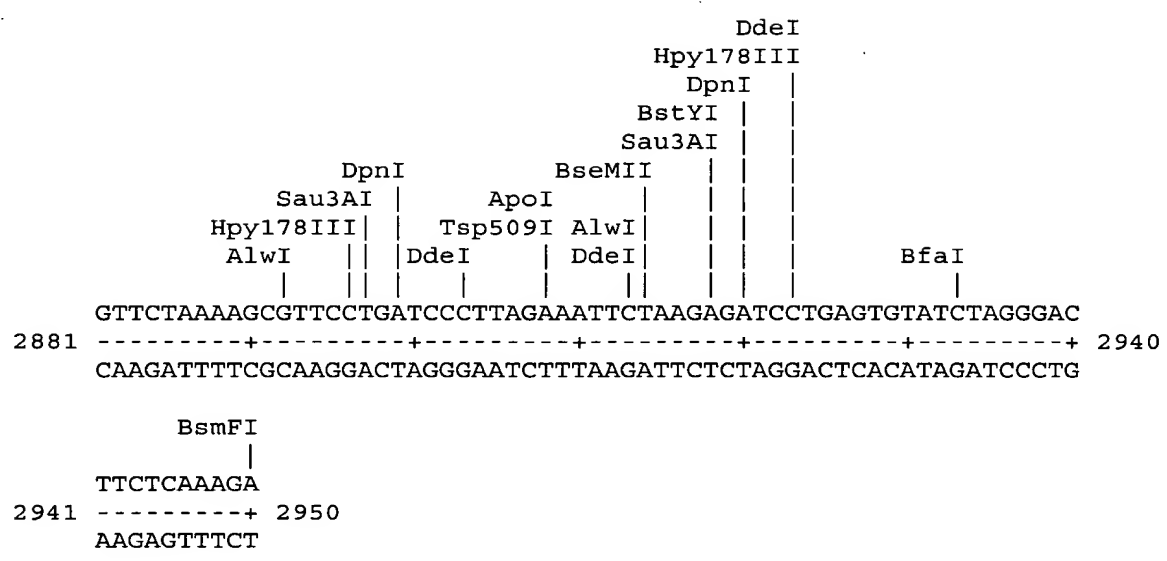




Fig. 6 L (cont)





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Figure 7 A: Nucleotide and amino acid sequence of CPN100639

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gtacgaagtt cttcacgaaa ttataataca aacctaggct ctaagttttg tttctagatt 60
atcgaaaacg tgtaatttaa ttgaacccaa gcattctttct atg aaa ata ccc ttg 115
                                         Met Lys Ile Pro Leu
                                         1           5

cac aaa ctc ctg atc tct tcg act ctt gtc act ccc att cta ttg agc 163
His Lys Leu Leu Ile Ser Ser Thr Leu Val Thr Pro Ile Leu Leu Ser
                        10                        15                        20

att gca act tac gga gca gat gct tct tta tcc cct aca gat agc ttt 211
Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser Pro Thr Asp Ser Phe
                        25                        30                        35

gat gga gcg ggc ggc tct aca ttt act cca aaa tct aca gca gat gcc 259
Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys Ser Thr Ala Asp Ala
                        40                        45                        50

aat gga acg aac tat gtc tta tca gga aat gtc tat ata aac gat gct 307
Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val Tyr Ile Asn Asp Ala
                        55                        60                        65

ggg aaa ggc aca gca tta aca ggc tgc tgc ttt aca gaa act acg ggt 355
Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe Thr Glu Thr Thr Gly
                        70                        75                        80                        85

gat ctg aca ttt act gga aag gga tac tca ttt tca ttc aac acg gta 403
Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe Ser Phe Asn Thr Val
                        90                        95                        100

gat gcg ggt tcg aat gca gga gct gcg gca agc aca act gct gat aaa 451
Asp Ala Gly Ser Asn Ala Gly Ala Ala Ala Ser Thr Thr Ala Asp Lys
                        105                        110                        115

gcc cta atc ttc aca gga ttt tct aac ctt tcc ttc att gca gct cct 499
Ala Leu Ile Phe Thr Gly Phe Ser Asn Leu Ser Phe Ile Ala Ala Pro
                        120                        125                        130

gga act aca gtt gct tca gga aaa agt act tta agt tct gca gga gcc 547
Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu Ser Ser Ala Gly Ala
                        135                        140                        145

tta aat ctt acc gat aat gga acg att ctc ttt agc caa aac gtc tcc 595
Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe Ser Gln Asn Val Ser
                        150                        155                        160                        165

aat gaa gct aat aac aat ggc gga gcg atc acc aca aaa act ctt tct 643
Asn Glu Ala Asn Asn Asn Gly Gly Ala Ile Thr Thr Lys Thr Leu Ser
                        170                        175                        180

att tct ggg aat acc tct tct ata acc ttc act agt aat agc gca aaa 691
Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr Ser Asn Ser Ala Lys
                        185                        190                        195
```



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Fig. 7 B (con't)

aaa tta ggt gga gcg atc tat agc tct gcg gct gca agt att tca gga	739
Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala Ala Ser Ile Ser Gly	
200 205 210	
aac acc ggc cag tta gtc ttt atg aat aat aaa gga gaa act ggg ggt	787
Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys Gly Glu Thr Gly Gly	
215 220 225	
ggg gct ctg ggc ttt gaa gcc agc tcc tcg att act caa aat agc tcc	835
Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile Thr Gln Asn Ser Ser	
230 235 240 245	
ctt ttc ttc tct gga aac act gca aca gat gct gca ggc aag ggc ggg	883
Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala Ala Gly Lys Gly Gly	
250 255 260	
gcc att tat tgt gaa aaa aca gga gag act cct act ctt act atc tct	931
Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro Thr Leu Thr Ile Ser	
265 270 275	
gga aat aaa agt ctg acc ttc gcc gag aac tct tca gta act caa ggc	979
Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser Ser Val Thr Gln Gly	
280 285 290	
gga gca atc tgt gcc cat ggt cta gat ctt tcc gct gct ggc cct acc	1027
Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser Ala Ala Gly Pro Thr	
295 300 305	
cta ttt tca aat aat aga tgc ggg aac aca gct gca ggc aag ggc ggc	1075
Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala Ala Gly Lys Gly Gly	
310 315 320 325	
gct att gca att gcc gac tct gga tct tta agt ctc tct gca aat caa	1123
Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Asn Gln	
330 335 340	
gga gac atc acg ttc ctt ggc aac act cta acc tca acc tcc gcg cca	1171
Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr Ser Thr Ser Ala Pro	
345 350 355	
aca tcg aca cgg aat gct atc tac ctg gga tcg tca gca aaa att acg	1219
Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser Ser Ala Lys Ile Thr	
360 365 370	
aac tta agg gca gcc caa ggc caa tct atc tat ttc tat gat ccg att	1267
Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr Phe Tyr Asp Pro Ile	
375 380 385	
gca tct aac acc aca gga gct tca gac gtt ctg acc atc aac caa ccg	1315
Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu Thr Ile Asn Gln Pro	
390 395 400 405	
gat agc aac tcg cct tta gat tat tca gga acg att gta ttt tct ggg	1363
Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr Ile Val Phe Ser Gly	
410 415 420	

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ANNOTATED SHEET SHOWING CHANGES  
Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF

Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128

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Fig. 7 C (cont.)

gaa aag ctc tct gca gat gaa gcg aaa gct gct gat aac ttc aca tct	1411
Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala Asp Asn Phe Thr Ser	
425 430 435	
ata tta aag caa cca ttg gct cta gcc tct gga acc tta gca ctc aaa	1459
Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly Thr Leu Ala Leu Lys	
440 445 450	
gga aat gtc gag tta gat gtc aat ggt ttc aca cag act gaa ggc tct	1507
Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr Gln Thr Glu Gly Ser	
455 460 465	
aca ctc ctc atg caa cca gga aca aag ctc aaa gca gat act gaa gct	1555
Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys Ala Asp Thr Glu Ala	
470 475 480 485	
atc agt ctt acc aaa ctt gtc gtt gat ctt tct gcc tta gag gga aat	1603
Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser Ala Leu Glu Gly Asn	
490 495 500	
aag agt gtg tcc att gaa aca gca gga gcc aac aaa act ata act cta	1651
Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn Lys Thr Ile Thr Leu	
505 510 515	
acc tct cct ctt gtt ttc caa gat agt agc ggc aat ttt tat gaa agc	1699
Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly Asn Phe Tyr Glu Ser	
520 525 530	
cat acg ata aac caa gcc ttc acg cag cct ttg gtg gta ttc act gct	1747
His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu Val Val Phe Thr Ala	
535 540 545	
gct act gct gct agc gat att tat atc gat gcg ctt ctc act tct cca	1795
Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala Leu Leu Thr Ser Pro	
550 555 560 565	
gta caa act cca gaa cct cat tac ggg tat cag gga cat tgg gaa gcc	1843
Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln Gly His Trp Glu Ala	
570 575 580	
act tgg gca gac aca tca act gca aaa tca gga act atg act tgg gta	1891
Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly Thr Met Thr Trp Val	
585 590 595	
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Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Ala Ser Val Val Pro	
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gat tca tta tgg gca tcc ttt act gac att cgc act cta cag cag atc	1987
Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg Thr Leu Gln Gln Ile	
615 620 625	
atg aca tct caa gcg aat agt atc tat cag caa cga gga ctc tgg gca	2035
Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln Arg Gly Leu Trp Ala	
630 635 640 645	



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Fig. 7.D (cont.)

tca gga act gcg aat ttc ttc cat aag gat aaa tca gga act aac caa	2083
Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys Ser Gly Thr Asn Gln	
650 655 660	
gca ttc cga cat aaa agc tac ggc tat att gtt gga gga agt gct gaa	2131
Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val Gly Gly Ser Ala Glu	
665 670 675	
gat ttt tct gaa aat atc ttc agt gta gct ttc tgc cag ctc ttc ggt	2179
Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe Cys Gln Leu Phe Gly	
680 685 690	
aaa gat aaa gac ctg ttt ata gtt gaa aat acc tct cat aac tat tta	2227
Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr Ser His Asn Tyr Leu	
695 700 705	
gcg tcg cta tac ctg caa cat cga gca ttc cta gga gga ctt ccc atg	2275
Ala Ser Leu Tyr Leu His Arg Ala Phe Leu Gly Gly Leu Pro Met	
710 715 720 725	
ccc tca ttt gga agt atc acc gac atg ctg aaa gat att cct ctc att	2323
Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys Asp Ile Pro Leu Ile	
730 735 740	
ttg aat gcc cag cta agc tac agc tac act aaa aat gat atg gat act	2371
Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys Asn Asp Met Asp Thr	
745 750 755	
cgc tat act tcc tat cct gaa gct caa ggc tct tgg acc aat aac tct	2419
Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser Trp Thr Asn Asn Ser	
760 765 770	
ggg gct cta gag ctc gga gga tct ctg gct cta tat ctc cct aaa gaa	2467
Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu Tyr Leu Pro Lys Glu	
775 780 785	
gca ccg ttc ttc cag gga tat ttc ccc ttc tta aag ttc cag gca gtc	2515
Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu Lys Phe Gln Ala Val	
790 795 800 805	
tac agc cgc caa caa aac ttt aaa gag agt ggc gct gaa gcc cgt gct	2563
Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly Ala Glu Ala Arg Ala	
810 815 820	
ttt gat gat gga gac cta gtg aac tgc tct atc cct gtc ggc att cgg	2611
Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile Pro Val Gly Ile Arg	
825 830 835	
tta gaa aaa atc tcc gaa gat gaa aaa aat aat ttc gag att tct cta	2659
Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn Phe Glu Ile Ser Leu	
840 845 850	
gcc tac att ggt gat gtg tat cgt aaa aat ccc cgt tcg cgt act tct	2707
Ala Tyr Ile Gly Asp Val Tyr Arg Lys Asn Pro Arg Ser Arg Thr Ser	
855 860 865	



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Fig. 7 E (con't)

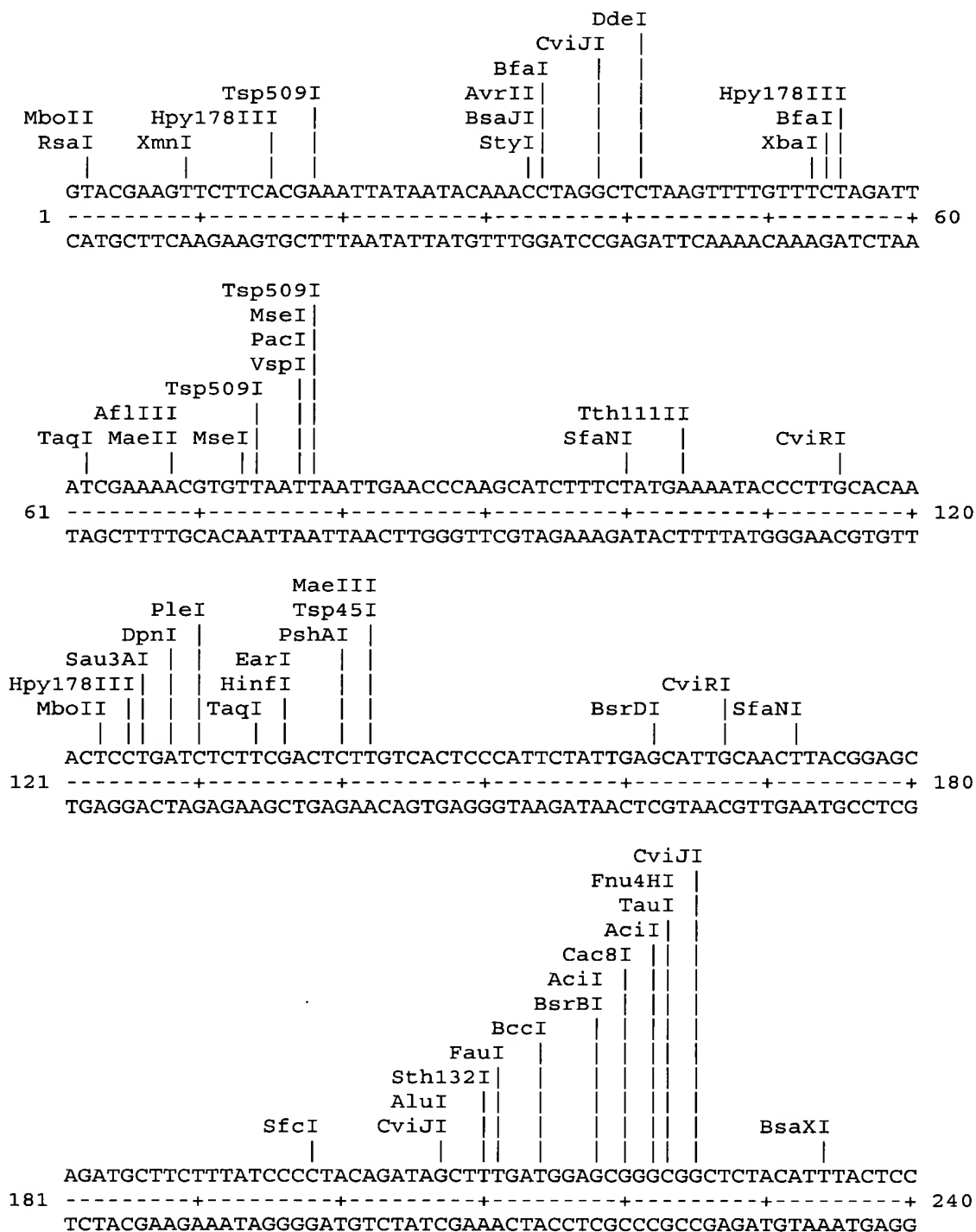
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cga caa gcc ttc tta gca agt gct gga agc cat ctg act ctc tcc cct	2803
Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His Leu Thr Leu Ser Pro	
890 895 900	
cat gta gaa ctc tct ggg gaa gct gct tat gag ctt cgt ggc tca gca	2851
His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu Leu Arg Gly Ser Ala	
905 910 915	
cac atc tac aat gta gat tgt ggg cta aga tac tca ttc tagttcctac	2900
His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr Ser Phe	
920 925 930	
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Inventor(s): Andrew D. MURDIN et al.  
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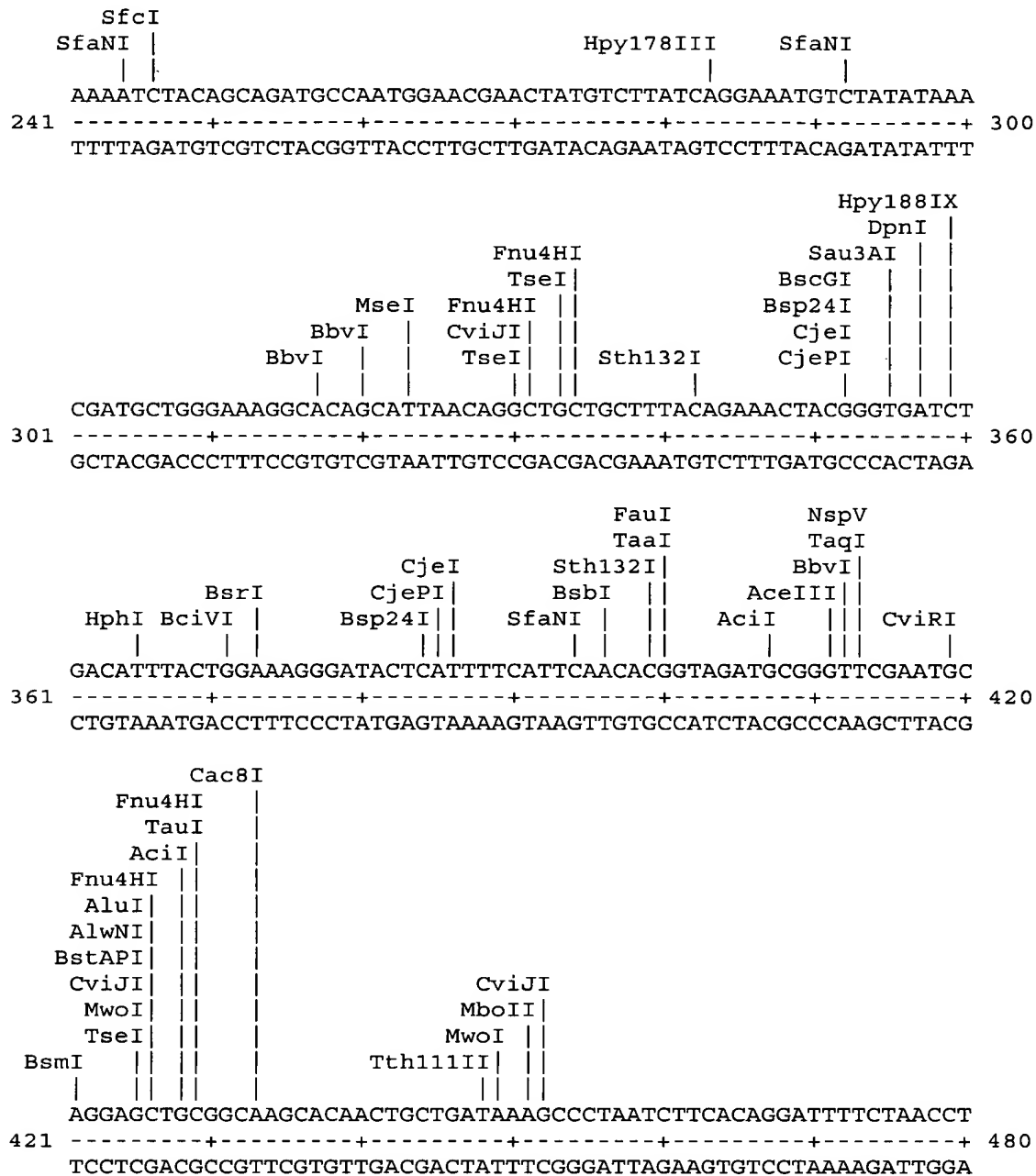
Figure 8 A: Restriction enzyme analysis of CPN100639





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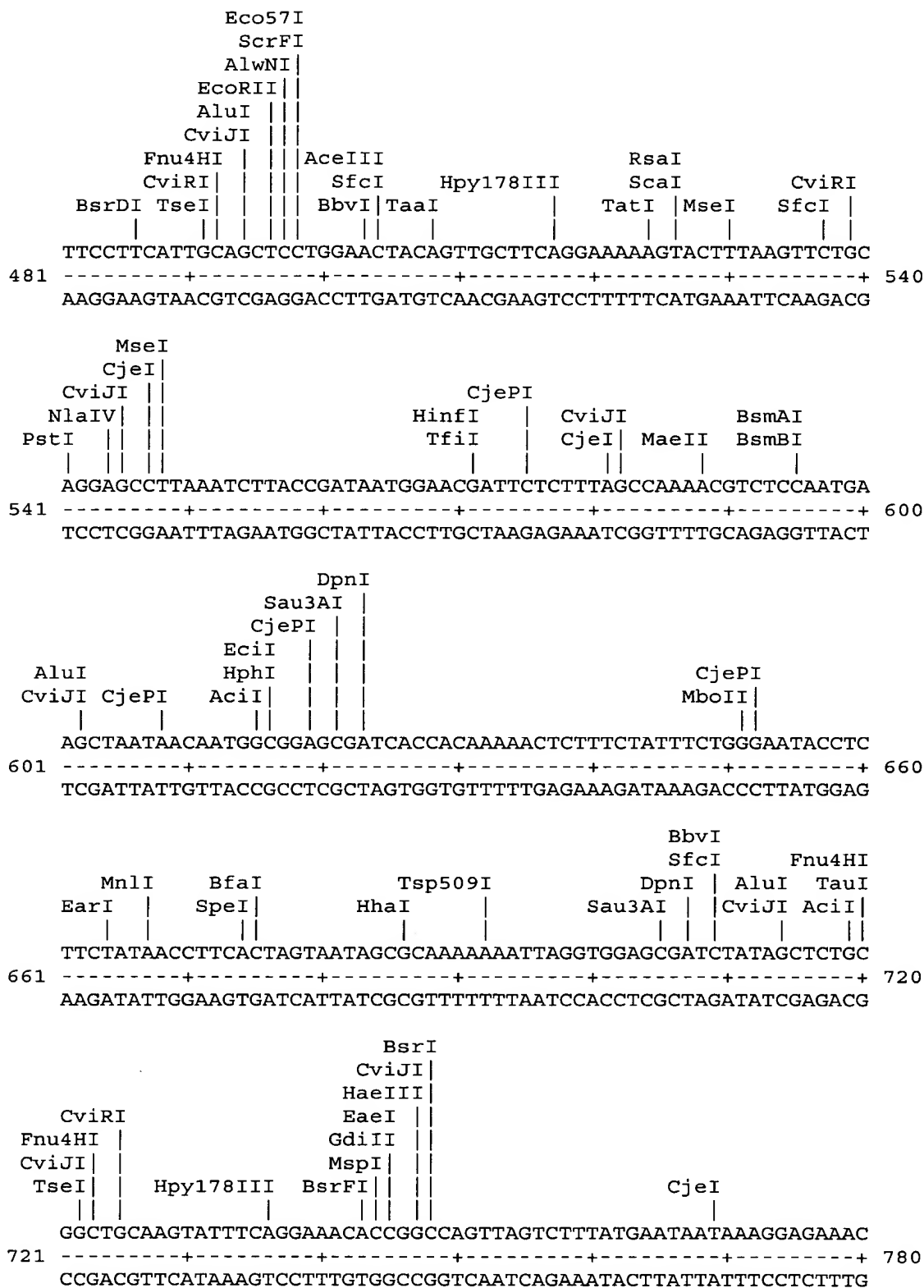
Fig. 8B (con't)





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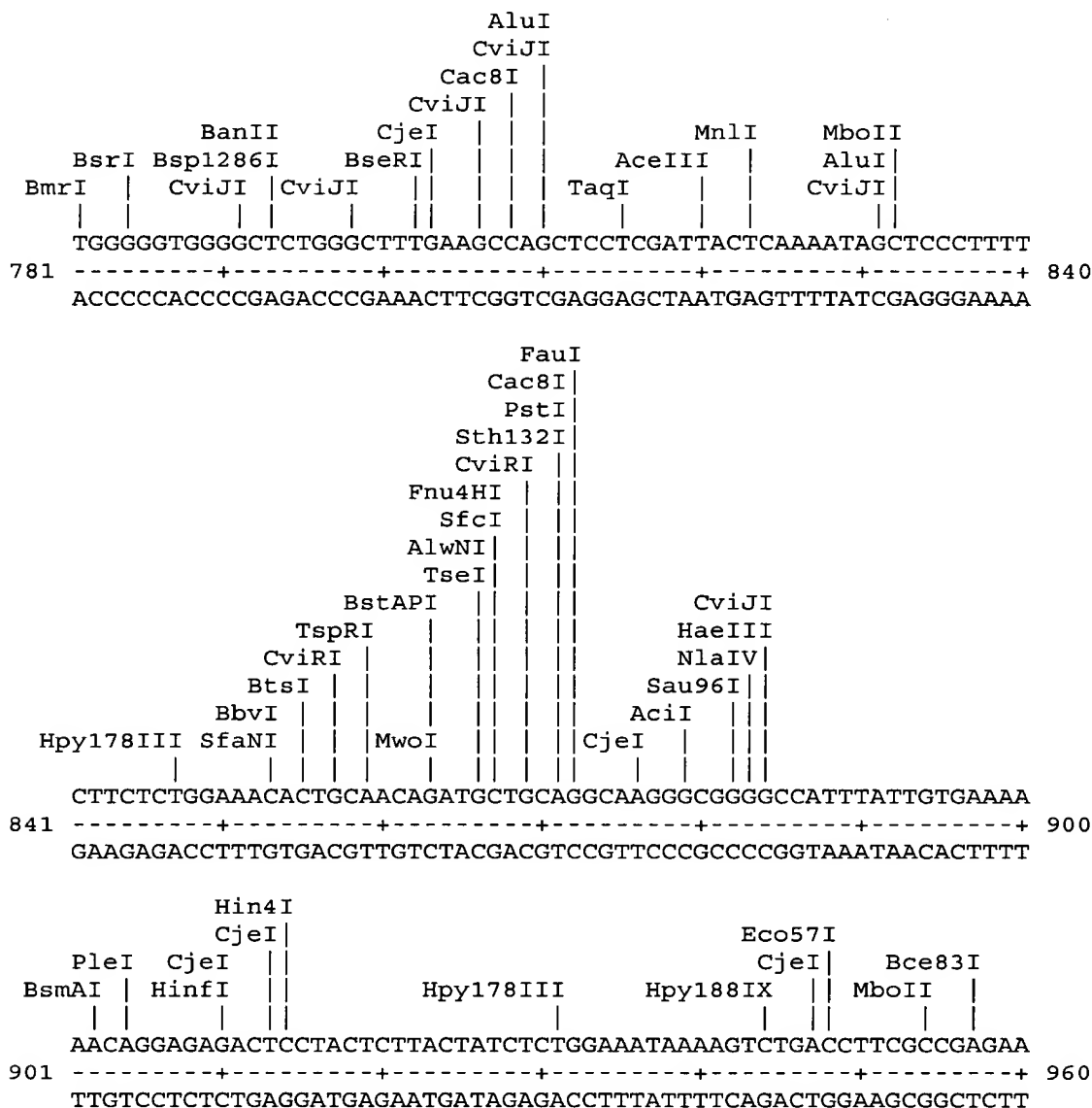
Fig. 8 C (con't)





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Fig. 8 D (cont.)

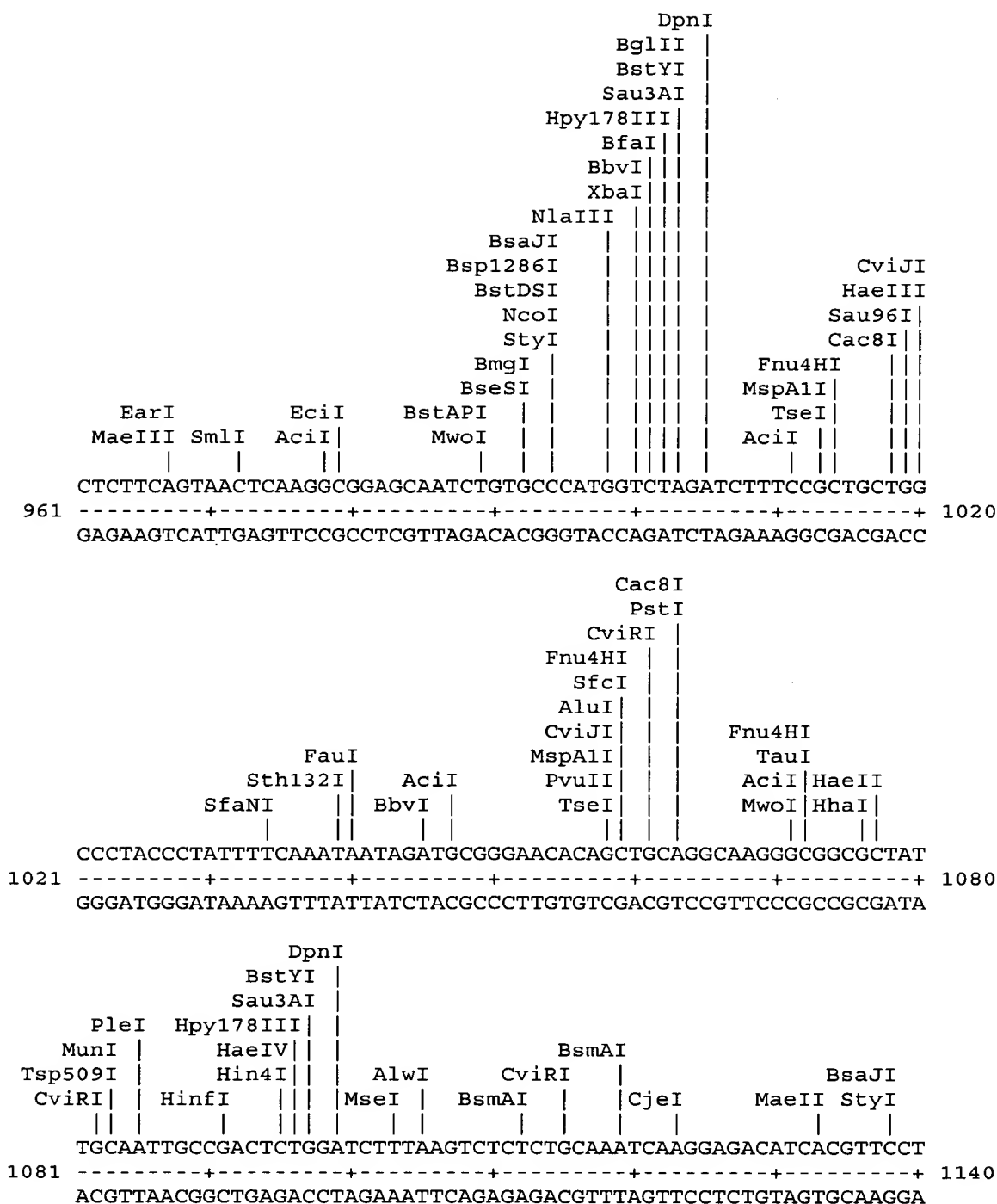






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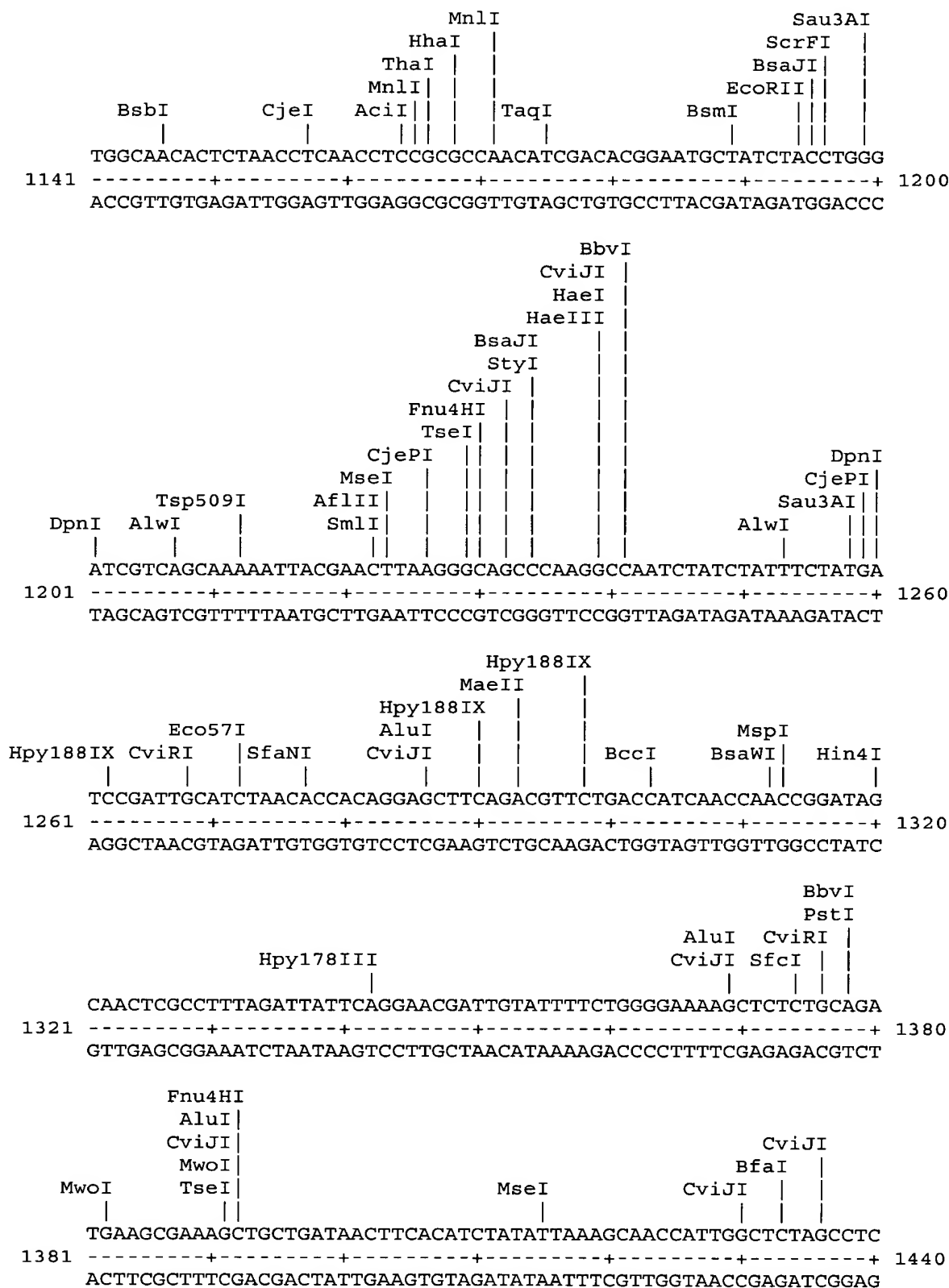
Fig. 8 E (con't)





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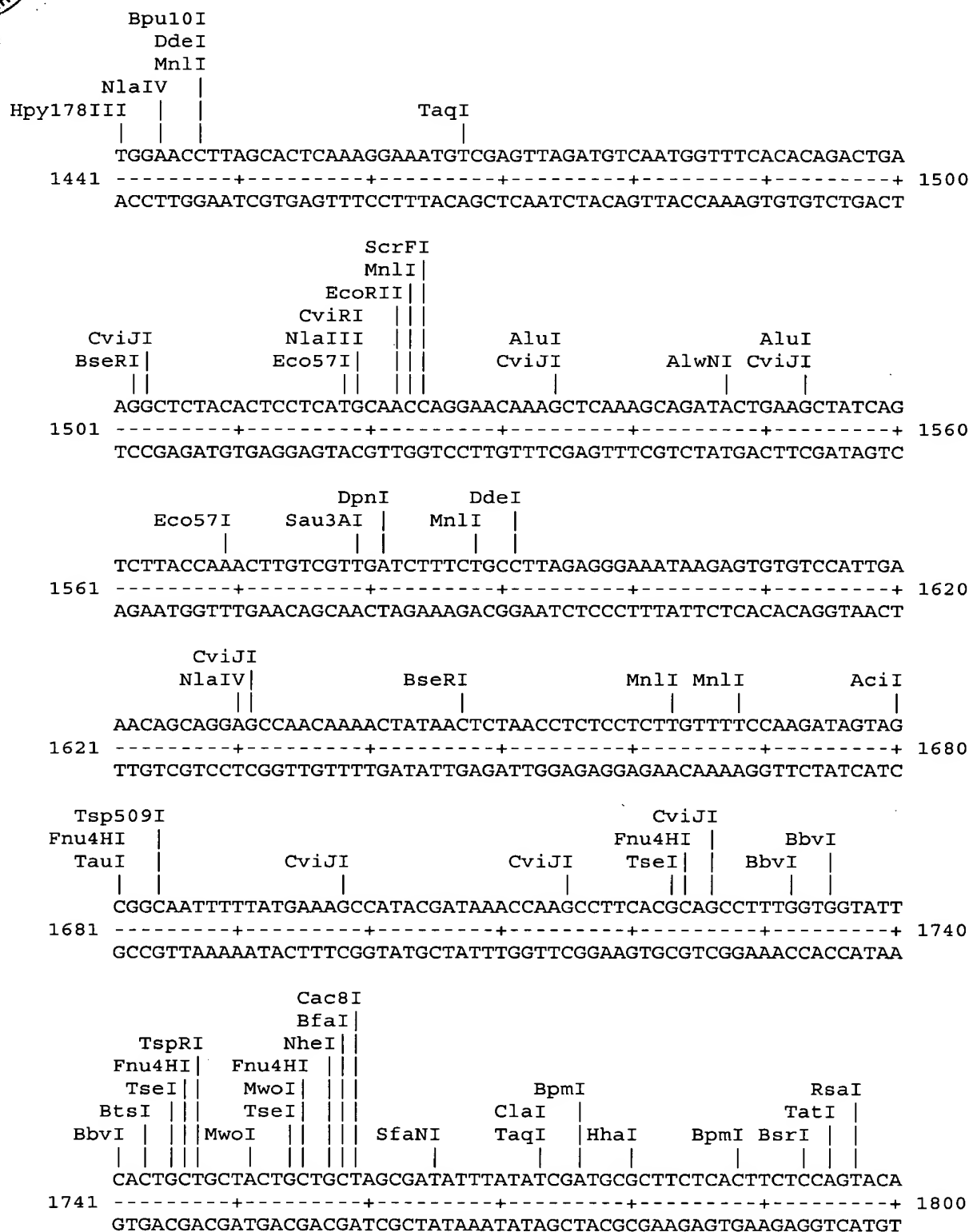
Fig. 8 F (con't)





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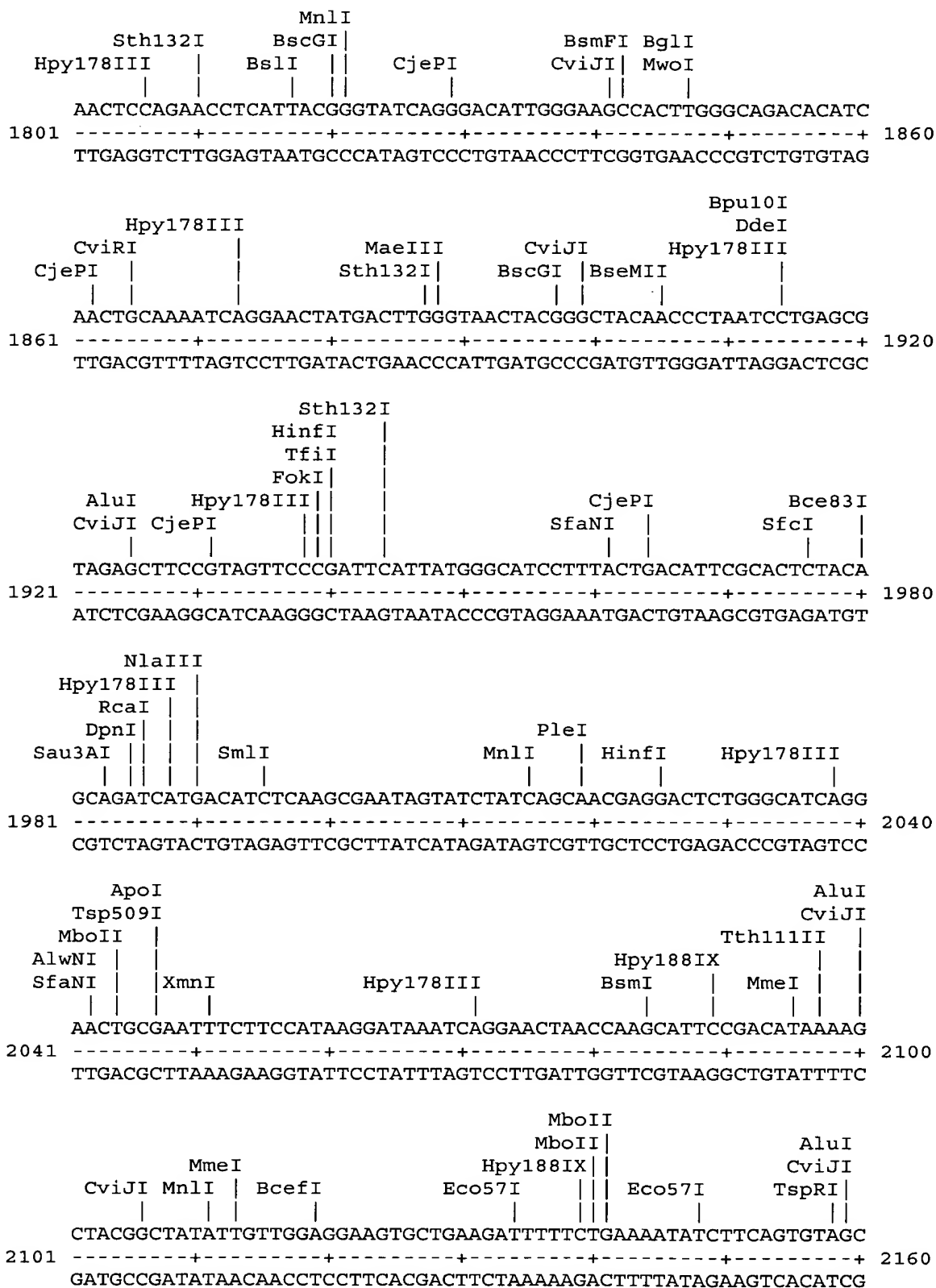
Fig. 8 ~~6~~ (con't)





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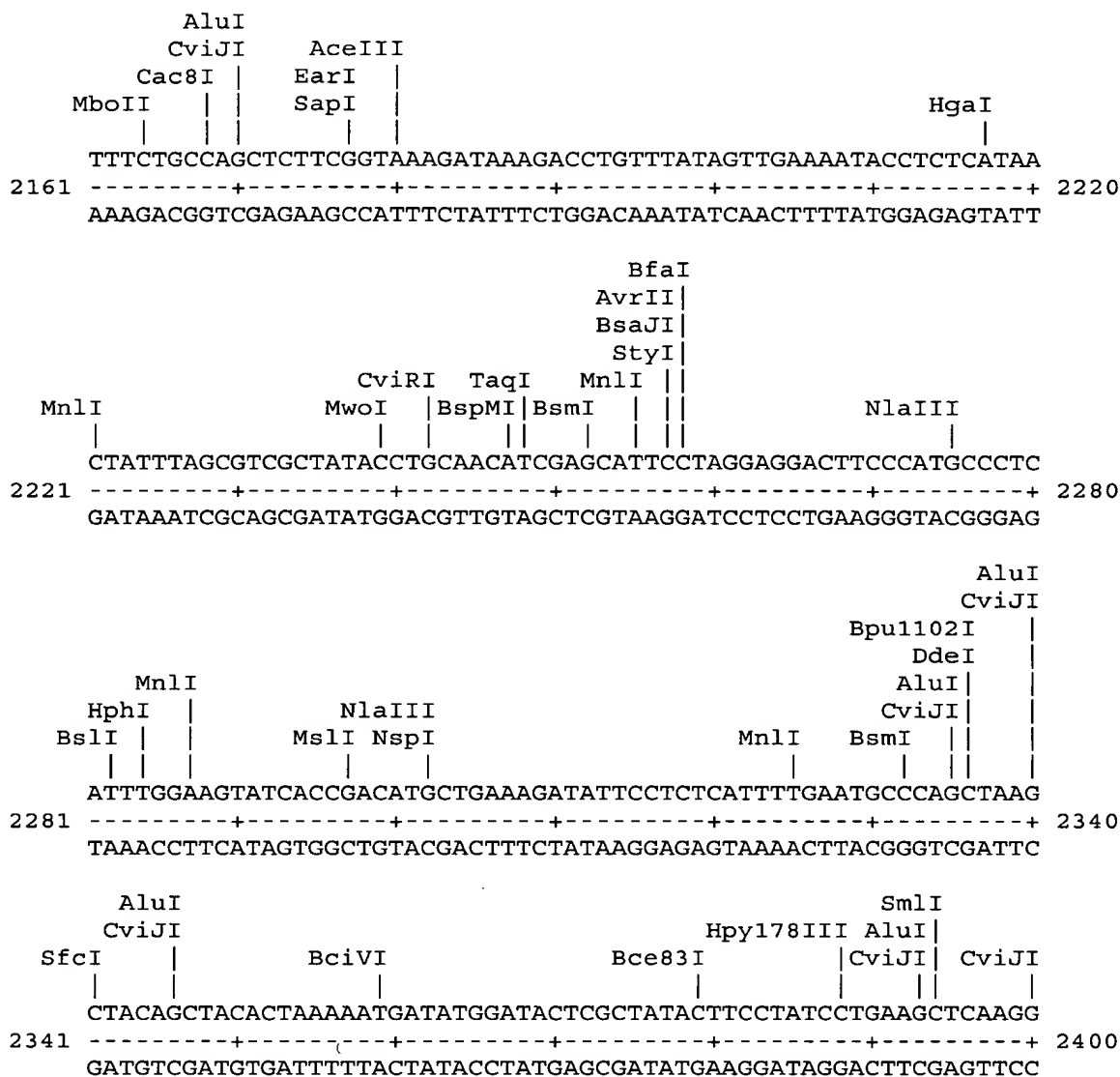
Fig. 8H (cont.)





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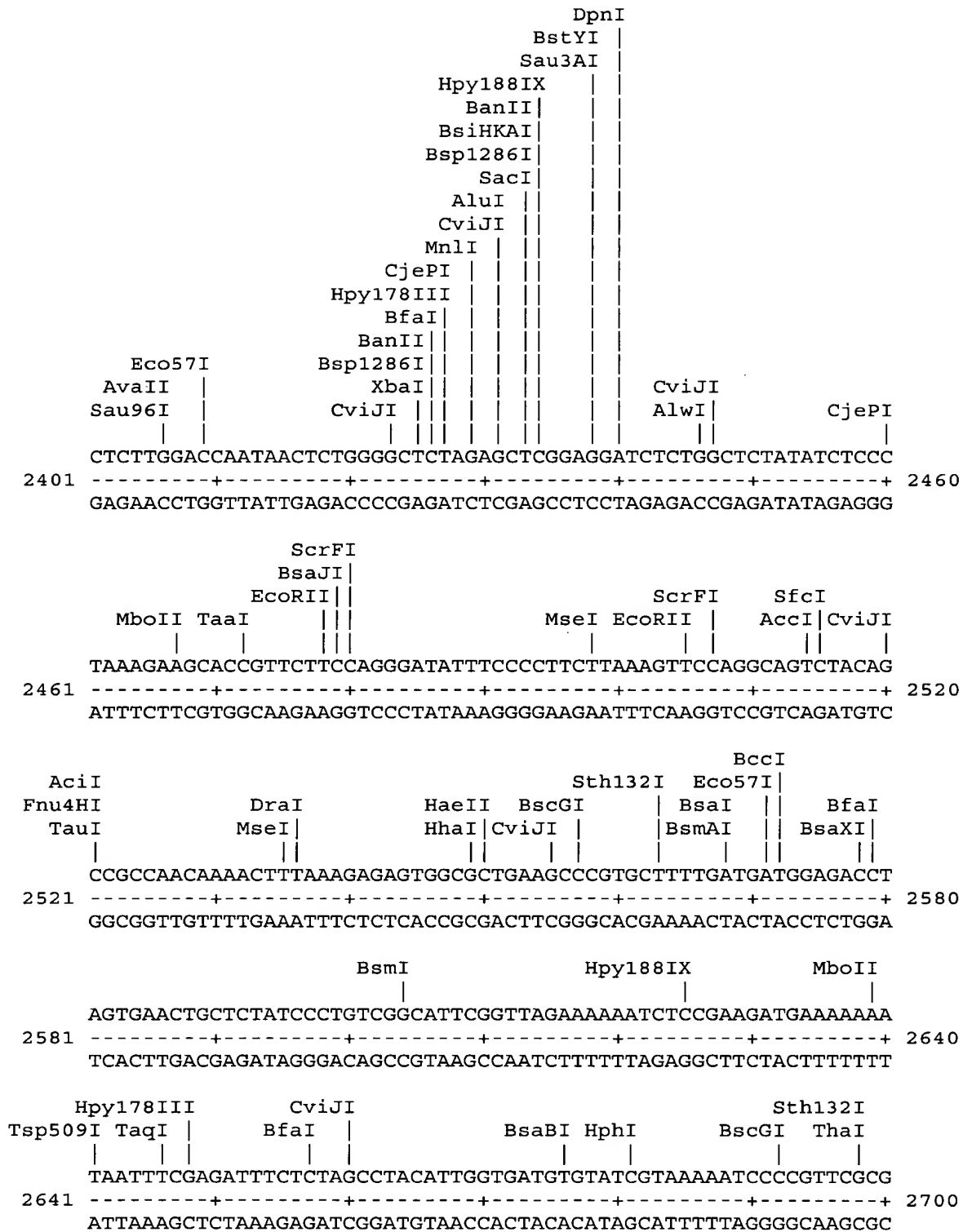
Fig. 81 (cont.)





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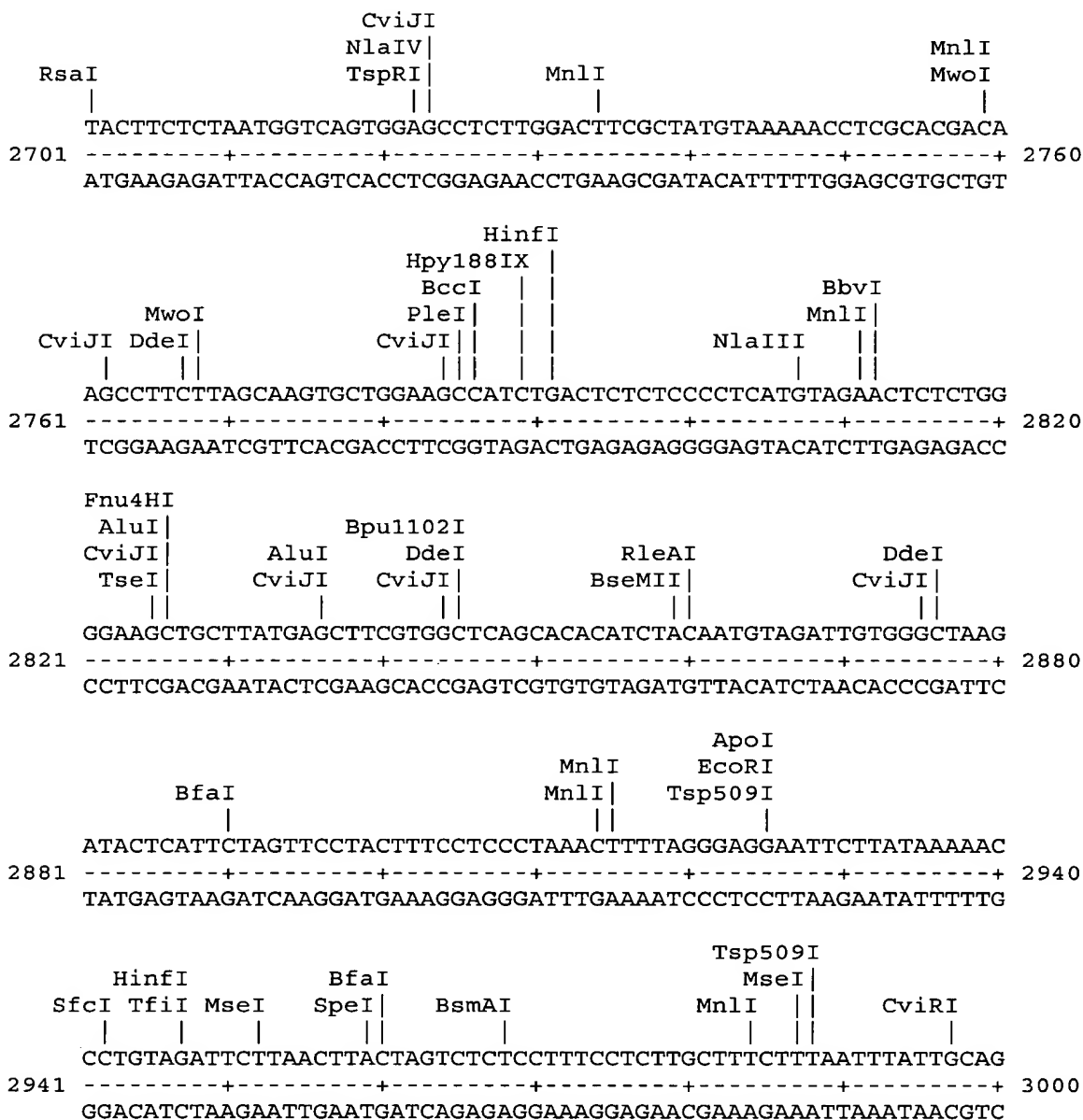
Fig. 8 J (cont.)





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Fig. 8 K (con't)





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Figure 9 A: Nucleotide and amino acid sequence of CPN100708

```
ataaagtttt ttatatgaac aaaactttga cttcattggc agacacttcg accttaacag 60
accaattttg ttgtcatccc tataaaaatc aggaattttc atg ctc tcc tca cta 115
                                         Met Leu Ser Ser Leu
                                         1           5
atc cgt gat tca ttt ccc ctt ctt att tta ctt ccc aca ttc cta gcg 163
Ile Arg Asp Ser Phe Pro Leu Leu Ile Leu Leu Pro Thr Phe Leu Ala
                        10                        15                        20
gca tta gga gcc tcc gta gct ggc ggc gtt atg gga acc tat atc gtt 211
Ala Leu Gly Ala Ser Val Ala Gly Gly Val Met Gly Thr Tyr Ile Val
                        25                        30                        35
gta aaa cgt att gtt tca att agt gga agt ata tct cat gca att cta 259
Val Lys Arg Ile Val Ser Ile Ser Gly Ser Ile Ser His Ala Ile Leu
                        40                        45                        50
gga gga att ggc ctc acc cta tgg ata caa tat aag ctt cat ctc tct 307
Gly Gly Ile Gly Leu Thr Leu Trp Ile Gln Tyr Lys Leu His Leu Ser
                        55                        60                        65
ttt ttc cct atg tat gga gct att gta gga gct att ttt cta gct ctt 355
Phe Phe Pro Met Tyr Gly Ala Ile Val Gly Ala Ile Phe Leu Ala Leu
                        70                        75                        80                        85
tgc atc ggc aag atc cac ctg aaa tac caa gaa agg gaa gac tct ttg 403
Cys Ile Gly Lys Ile His Leu Lys Tyr Gln Glu Arg Glu Asp Ser Leu
                        90                        95                        100
att gcg atg att tgg tct gtg ggc atg gca att gga att ata ttc att 451
Ile Ala Met Ile Trp Ser Val Gly Met Ala Ile Gly Ile Ile Phe Ile
                        105                        110                        115
tcc agg ctt ccc acc ttt aat gga gag ctc atc aat ttt cta ttt ggg 499
Ser Arg Leu Pro Thr Phe Asn Gly Glu Leu Ile Asn Phe Leu Phe Gly
                        120                        125                        130
aac att ctc tgg gtc acc cct tca gac ctc tat agc tta gga atc ttt 547
Asn Ile Leu Trp Val Thr Pro Ser Asp Leu Tyr Ser Leu Gly Ile Phe
                        135                        140                        145
gat ctt ctt gtt tta gga att gtg gtc ctt tgc cac acc cgg ttc ctt 595
Asp Leu Leu Val Leu Gly Ile Val Val Leu Cys His Thr Arg Phe Leu
                        150                        155                        160                        165
gct ctt tgc ttt gat gag agg tac acg gct tta aac cat tgt tct gta 643
Ala Leu Cys Phe Asp Glu Arg Tyr Thr Ala Leu Asn His Cys Ser Val
                        170                        175                        180
cag ctg tgg tat ttc cta ctt ctt gtt ctg aca gca atc acg att gtg 691
Gln Leu Trp Tyr Phe Leu Leu Leu Val Leu Thr Ala Ile Thr Ile Val
                        185                        190                        195
```





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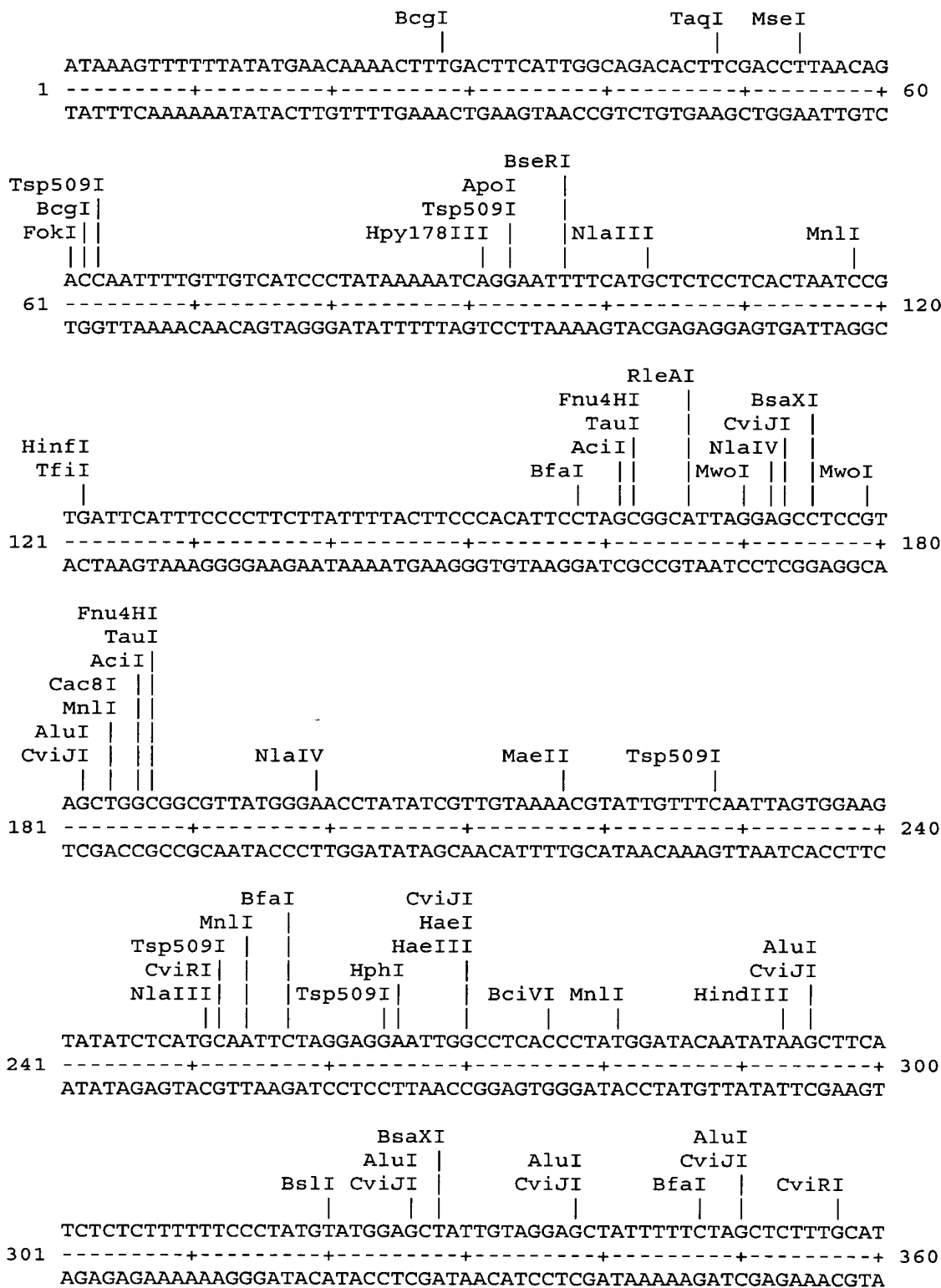
Fig. 9 B (con't)

atg ttg att tat gtg atg gga acg att ctg atg ctt agc atg ctc gtc	739
Met Leu Ile Tyr Val Met Gly Thr Ile Leu Met Leu Ser Met Leu Val	
200 205 210	
tta cct gtt gct ata gcg tgt aga ttt tcg tac aag atg aca cga att	787
Leu Pro Val Ala Ile Ala Cys Arg Phe Ser Tyr Lys Met Thr Arg Ile	
215 220 225	
atg ttc atc tcg gtc ctc ttg aat atc tta tgt tct ttt tct gga att	835
Met Phe Ile Ser Val Leu Leu Asn Ile Leu Cys Ser Phe Ser Gly Ile	
230 235 240 245	
tgc atc gcc tac tgt tta gat ttc cca gta ggt cct acg ata tca ttg	883
Cys Ile Ala Tyr Cys Leu Asp Phe Pro Val Gly Pro Thr Ile Ser Leu	
250 255 260	
ctg atg ggg tta ggt tat aca gcg agt ctt tgt gtg aag aag cgg tac	931
Leu Met Gly Leu Gly Tyr Thr Ala Ser Leu Cys Val Lys Lys Arg Tyr	
265 270 275	
aat ccg tcg acg cct tct cct gta agt cct gaa atc aat aca aat gta	979
Asn Pro Ser Thr Pro Ser Pro Val Ser Pro Glu Ile Asn Thr Asn Val	
280 285 290	
tagctagggga agcgcttttg gaagctttgg aggcattctt cctgttcgtc aggaagaaga	1039
tcatacaattt tatttaaagc taccagcata tctttctttt caaaatctgg ctgatgagag	1099
t	1100



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Figure 10 A: Restriction enzyme analysis of CPN100708





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Fig. 10 B (cont)

```

      DpnI
      BstYI |
      Sau3AI |
      SfaNI |
      AlwI |
      PleI | BbsI |
      BslI | HinfI | MboII | RleAI |
      CGGCAAGATCCACCTGAAATACCAAGAAAGGGAAGACTCTTTGATTGCGATGATTGGTGC
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
      GCCGTTCTAGGTGGACTTTTATGGTTCTTTCCCTTCTGAGAACTAACGCTACTAAACCAG

      BanII
      BsiHKAI
      Bsp1286I
      SacI
      Tsp509I | CviJI |
      MunI | CjeI |
      Tsp509I | ScrFI |
      NlaIII | EcoRII | MseI |
      TGTGGGCATGGCAATTGGAATTATATTCATTTCCAGGCTTCCCACCTTTAATGGAGAGCT
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
      ACACCCGTACCGTTAACCTTAATATAAGTAAAGGTCCGAAGGGTGGAAATTACCTCTCGA

      HinfI
      MnlI |
      Bpu10I |
      DdeI |
      CjeI |
      BstEII |
      MaeIII |
      HphI | SimI |
      Tsp509I | Eco57I | Tsp45I | Hpy188IX | SfcI | CviJI | TfiI |
      CATCAATTTTCTATTGGAACATTCTCTGGGTACCCCTTCAGACCTCTATAGCTTAGG
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
      GTAGTTAAAGATAAACCTTGTAAAGAGACCCAGTGGGGAAGTCTGGAGATATCGAATCC

      Sth132I
      NlaIV |
      DpnI |
      Sau3AI |
      MboII |
      AvaII |
      CjeI |
      Tsp509I | Sau96I |
      MspI |
      NciI |
      ScrFI |
      AATCTTTGATCTTCTTGTTTTAGGAATTGTGGTCCTTTGCCACACCCGGTTCCTTGCTCT
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
      TTAGAAACTAGAAGAACAAAATCCTTAACACCAGGAAACGGTGTGGGCCAAGGAACGAGA

      AluI
      CviJI
      MspAII
      PvuII
      RsaI |
      DraI |
      BsrGI |
      MseI |
      TatI |
      MnlI |
      CjeI |
      RsaI | CviJI | BceFI |
      TTGCTTTGATGAGAGGTACACGGCTTTAAACCATTGTTCTGTACAGCTGTGGTATTTTCCT
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
      AACGAAACTACTCTCCATGTGCCGAAATTTGGTAACAAGACATGTCGACACCATAAAGGA
```

ANNOTATED SHEET SHOWING CHANGES  
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CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF  
Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128



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Inventor(s): Andrew D. MURDIN et al.  
Appl. No.: 09/857,128

Fig. 10 D (cont)

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          BfaI      HaeII      AluI
          AluI      HhaI      CviJI      BsmI
          Eco47III  MnlI      MwoI
          CviJI      MwoI      HindIII  MboII
          ||         ||         ||         ||
TGAAATCAATACAAATGTATAGCTAGGGAAGCGCTTTTGGAAGCTTTGGAGGCATTCTTC
961 -----+-----+-----+-----+-----+-----+-----+ 1020
ACTTTAGTTATGTTTACATATCGATCCCTTCGCGAAAACCTTCGAAACCTCCGTAAGAAG

          MboII
          MboII      AluI
          Tsp509I      CviJI
          DpnI      DraI
          Hpy178III  Sau3AI  MseI
          ||         ||         ||         ||
CTGTTTCGTCAGGAAGAAGATCATCAATTTTATTTAAAGCTACCAGCATATCTTTCTTTTC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
GACAAGCAGTCCTTCTTCTAGTAGTTAAAATAAATTCGATGGTCGTATAGAAAGAAAAG

          CviJI
          |
AAAATCTGGCTGATGAGAGT
1081 -----+-----+-----+ 1100
TTTTAGACCGACTACTCTCA
```